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FIG. 1

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

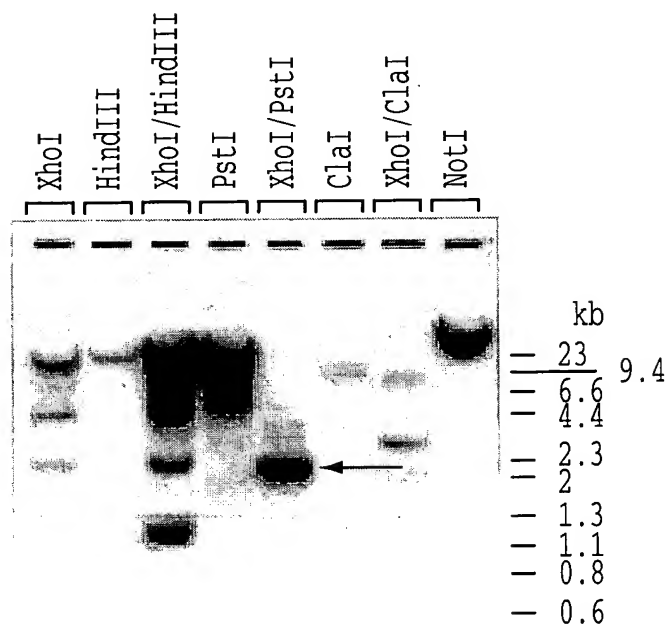
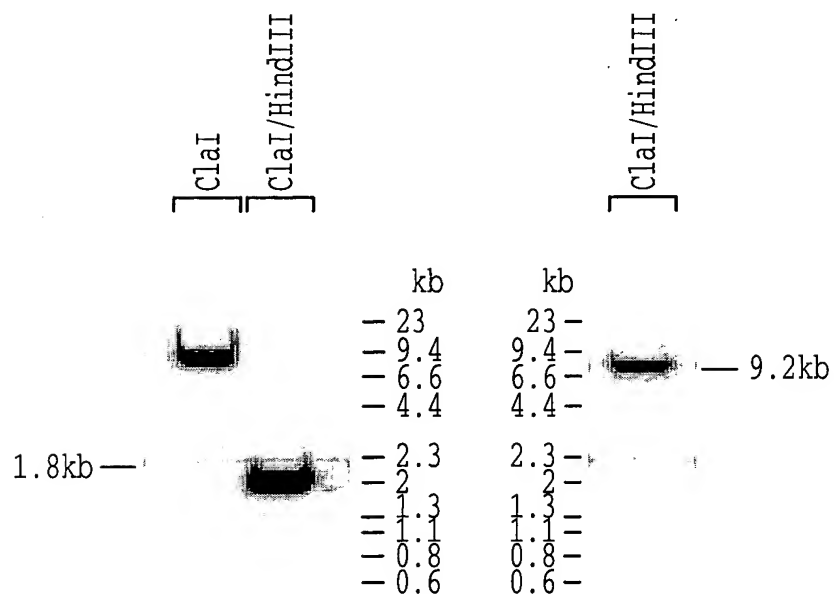


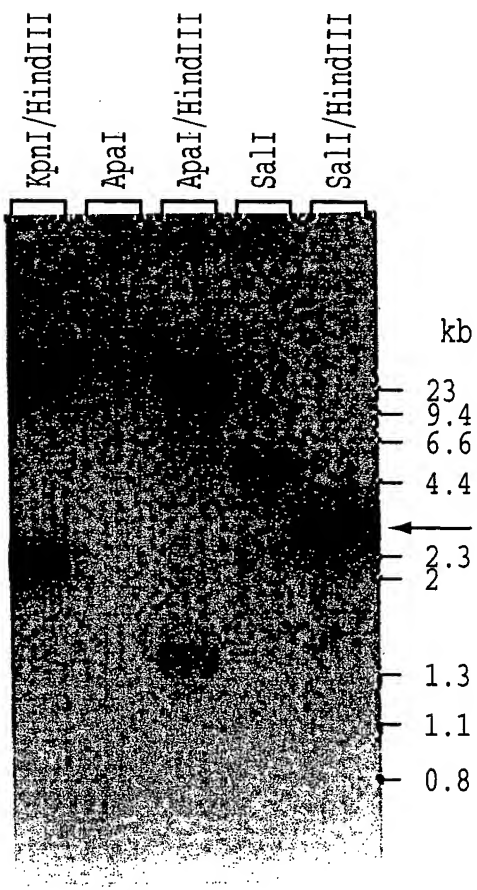
FIG. 2



**FIG. 3A**

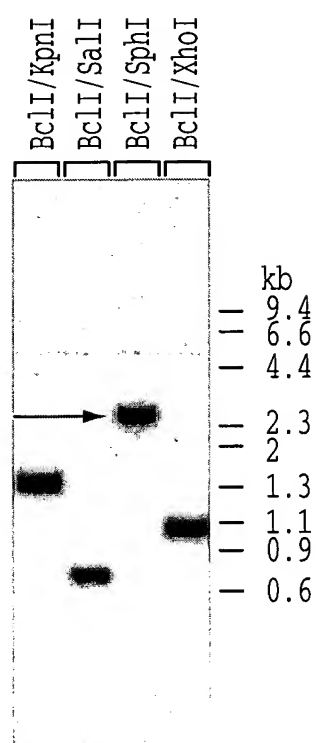
**FIG. 3B**

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PRODUCTION**



**FIG. 4**

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Parent Serial No.: 09/920,923  
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PRODUCTION**



**FIG. 5**

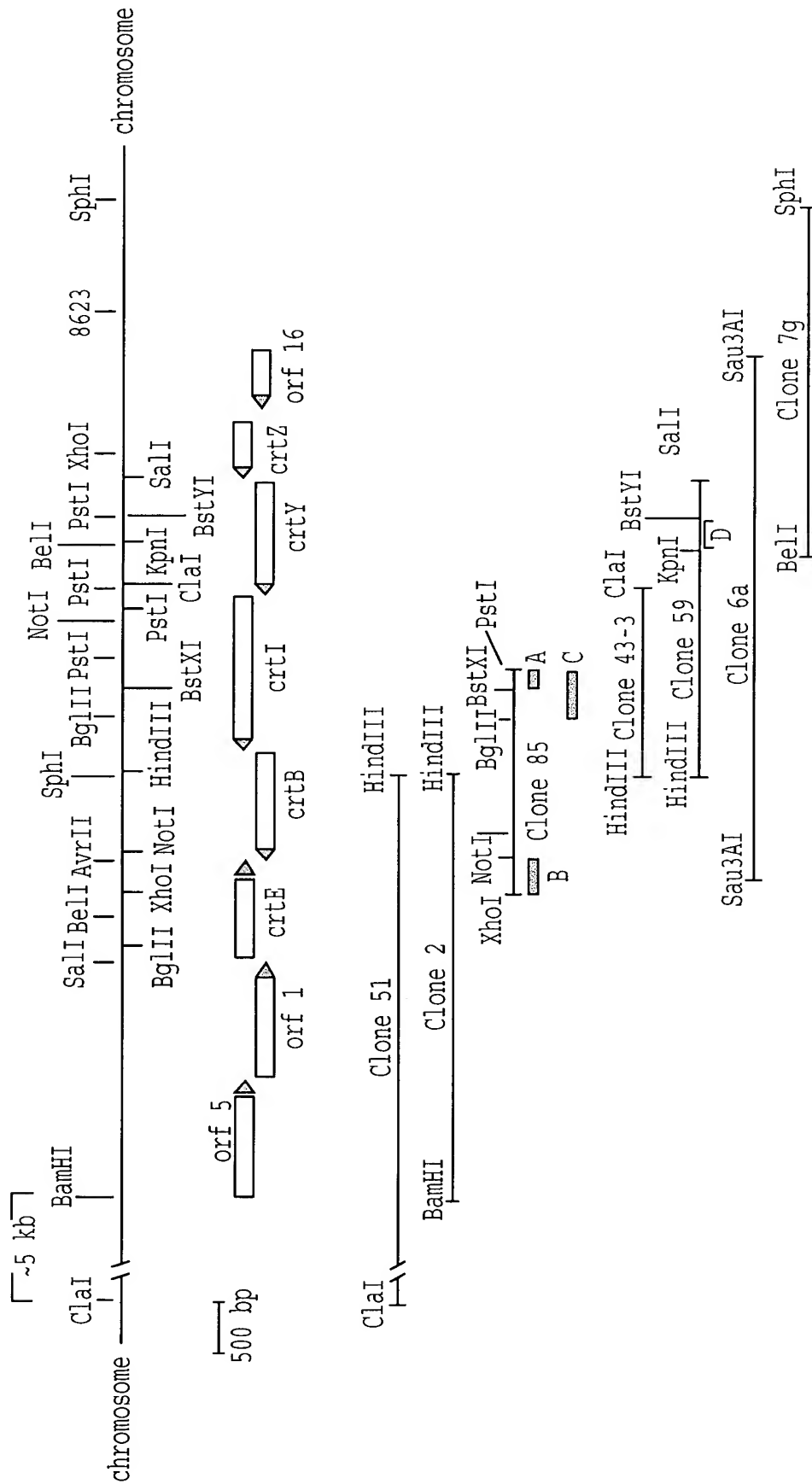


FIG. 6

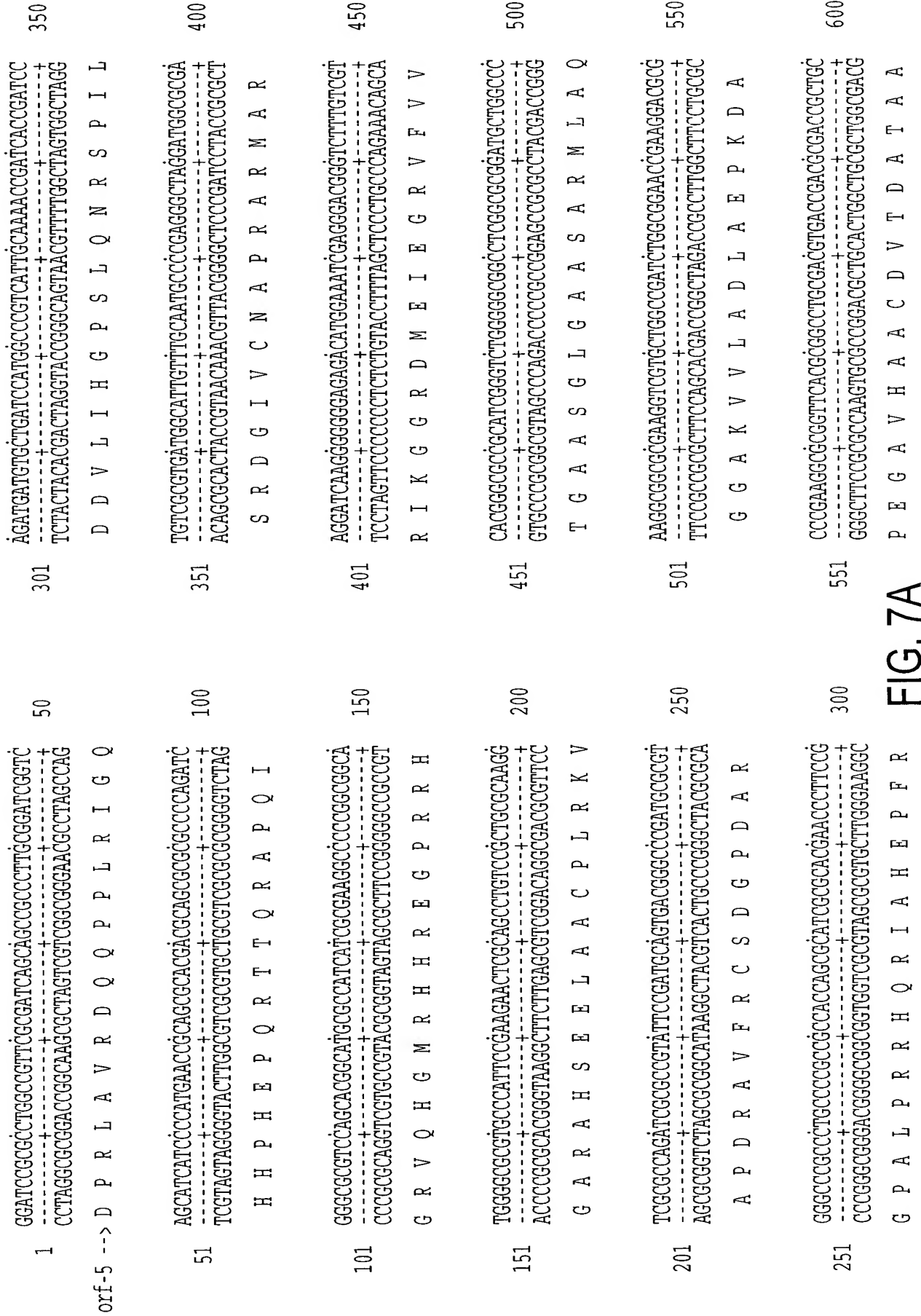


FIG. 7A

601	GCAGACGGCCATCGCGCTGGCGACCGACCGCCTTCGGCAGGCTGGAGGGC -----+-----+-----+-----+-----+ CGTCTGCCGTAGCGCGACCGCTGGCTGGCGAAGCGTCCGACCTGCGCG Q T A I A L A T D R F G R L D G L	650	901	CGTGGCGGGAATGACGCTGCGATGGCCCGCGACCTTGCGCGGACGGCA -----+-----+-----+-----+-----+ GCACCGCCCGTACTCGGACGCTACCGGGCGTGGAAACGCGCCGTGCGGT V A G M T L P M A R D L A R H G I	950
651	TTGTGAATGCGCGGGCATGCGCGCGCGCGGCGAACGGATGCTGGGCGCGGAC -----+-----+-----+-----+-----+ AACACTTACGCGCCCGTAGCGCGCGCGCTTGCTTACGACCGCGCGCTG V N C A G I A P A E R M L G R D	700	951	TCCCGCTATGACCATCGCGCGCGCGCATCTTCGCGACCCCGATGCTGGAG -----+-----+-----+-----+-----+ AGCGCAGTACTGTGTAGCGCGCGCGCGGTAGAAAGGCTGGGCTACGACCTC R V M T I A P G I F R T P M L E	1000
701	GGCGCGCATGGA CTGGACAGCTTTGCCCCGTCGGGTACGATCAACCTGAT -----+-----+-----+-----+-----+ CCCGGCTACTGACCTGTGGAACCGGGCAGCCAGTGTCTAGTTGGACTA G P H G L D S F A R A V T I N L I	750	1001	GGGCTGCCGAGGACCTTCAGACAGCCTGGCGCGCGGTGCCCTTCCC -----+-----+-----+-----+-----+ CCCCAGGCGCTCTCTGCAAGTCTCTGCGACCCGCGCGCGACGGGAAGG G L P Q D V Q D S L G A A V P F P	1050
751	CGGCAGCTTCAACATGGCCCGCTTGAGCGGAGGCGATGGCCCGGAACG -----+-----+-----+-----+-----+ GCGTCTGAAGTTGTACCGGCGGAACGTGCGCTCCGCTACCGGGCCCTTGC G S F N M A R L A A E A M A R N E	800	1051	CTCGCGGCTGGAGAGCGCGTCGGAATAGCGGCGCTGTTCACACCATCA -----+-----+-----+-----+-----+ GAGCGCCGACCTCTCGCGAGCCTTATGCGCCGCGACAACTGGTGTAGT S R L G E P S E Y A A L L H H I I	1100
801	AGCCCGTCCGGGCGAGCGTGGGTGATCGTCAACACAGGCTTCGATCGCG -----+-----+-----+-----+-----+ TCGGGCAGCCCCGCTCGCACCGCACTAGCAGTTGTCCGGAGCTAGCGC P V R G E R G V I V N T A S I A	850	1101	TCGCGAACCCATGCTGAAAGGAGAGGTATCCGCGCTCGAGCGCGCATTG -----+-----+-----+-----+-----+ AGCGCTGGGTACGACTGCTGCTCTCCAGTAGGCGGAGTCCCGGTAAAC A N P M L N G E V I R L D G A L	1150
851	GCGCAGGACGACATCGGACAGGTGCGCTATGCGCGCGAGCGAGCGGG -----+-----+-----+-----+-----+ CGGCTCCTGCTGTAGCCTGTCCAGCGGATACGCGGTGCTTCCGCGC A Q D G Q I G Q V A Y A A S K A G	900	1151	CGCATGGCCCCAAGTAGGAGGTTTCATGGACCCCATCGTCATCACCC -----+-----+-----+-----+-----+ GCGTACGGGGGTTCACTTCTCCGAAAGTACCTTGGGGTAGCAGTAGTGG R M A P K * M D P I V I T orf-1 -->	1200

**FIG. 7B**



1201	GGCGCGATGCGACCCCGAATGGGGCATTCAGGGCGAATTTGCCCGGAT -----+-----+-----+-----+-----+ CCGGGTACGGGTGGGGTACCCCGTAAGTCCGCTAGAACCGGGCTA G A M R T P M G A F Q G D L A A M	1250	1501	GTCTGCCCGGGGATGGAGACATGTGACGCCCCCTACCTGTGCCC -----+-----+-----+-----+-----+ CAGCAGCGGCGCGCTACCTCTCGTACAGCTTGCGGGGGATGGACGACGG V V A G G M E S M S N A P Y L L P	1550
1251	GGATGCCCCGACCTTTGGCGGGACGGGATCCGGCGCGCCTGAACGGCC -----+-----+-----+-----+-----+ CCTACGGGGCTGGGAACCGCGCCTGCGCTAGGGCGGGCGGACCTTGCCGG D A P T L G A D A I R A A L N G L	1300	1551	CAAGGCGCGTGGGGATGCGCATGGGCCATGACCGTGTGTGGATCACÀ -----+-----+-----+-----+-----+ GTTCCGCGCCAGCCCCCTACGCGTACCCGGTACTGGCACACACACCTAGTGT K A R S G M R M G H D R V L D H M	1600
1301	TGTGCCCCGATGTGGAACGAGGTGCTGATGGGTGCGTCTCGCCGCG -----+-----+-----+-----+-----+ ACAGCGGGCTGTACCACTGTCTACGACTACCGACGACGAGGAGCGGCGC S P D M V D E V L M G C V L A A	1350	1601	TGTTCTCGAGCGGGTTGGAGGAGCGCCTATGACAAAGGCCCGCTGATGGGC -----+-----+-----+-----+-----+ ACAAGAGCTGCCCCAACCTCTCGGATAGTGTTCGCGGCGACTACCCG F L D G L E D A Y D K G R L M G	1650
1351	GGCCAGGTTAGGACACCGGACAGTCAGGCGCGGCTTGGCGCCGGACTGCC -----+-----+-----+-----+-----+ CCGFTCCAGTCCGTGGCCGTGAGTCCGCGCGGAACCGCGGCCTGACGG G Q G Q A P A R Q A A L G A G L P	1400	1651	ACCTTCGCCGAGGATTGCGCGCGGATCAGGTTTCACCCGCGAGGCGCA -----+-----+-----+-----+-----+ TGAAGCGGCTCTCTAACCGGCGCGCTAGTCCAAAGTGGCGCTCCCGGT T F A E D C A G D H G F T R E A Q	1700
1401	GCTGTGACGGGACGACCAACATCAACGAGATGTGCGGATCGGGCATGA -----+-----+-----+-----+-----+ CGACAGTGCCTGCTGCTGGTGGTGTGCTCTACAGCCCTAGCCCCGTACT L S T G T T I N E M C G S G M K	1450	1701	GGACGACTATGCGCTGACCAAGCCTGGCCCGCGGAGGACGCCATCGCCA -----+-----+-----+-----+-----+ CCTGTGATACGCGACTGTCGAGACCGGGCGCGCTCCTGCGGTAGCGGT D D Y A L T S L A R A Q D A I A S	1750
1451	AGGCCGGAATGTGGGCCATGACCTGATCGCCGGGATCGCGGGCATC -----+-----+-----+-----+-----+ TCCGGGCTACGACCCGGTACTGGACTAGCGGGCCCTAGCGGCCCGCTAG A A M L G H D L I A A G S A G I	1500	1751	CGGGTGCCCTTCGCGCCCGAGATCGCGCCCGGTGACCCGTCAAGGACGCAAG -----+-----+-----+-----+-----+ CGCCACGGAAGCGCGGCTCTAGCGGGGCACTGGCAGTGCCTGCGTTC G A F A A E I A P V T V T A R K	1800

**FIG. 7C**

1801	GTGCAGACCACCGTGGATACCGAGAGATGCCCGGCAAGCCCCCGCCCGA -----+-----+-----+-----+-----+ CAGCTCTGGTGGCAGCTATGGCTGCTCTACGGGCGGTTCCGGGGCGGGCT V Q T T V D T D E M P G K A R P E	1850	2101	TAGGACCTGTTCCAGGTGAACGAGGCATTCCCGCTCGTCGCCATGATCGC -----+-----+-----+-----+-----+ ATGCTGGACAAGCTCCACTTGCTCCGTAAGCGGCAGCAGCGGTACTAGCG Y D L F E V N E A F A V V A M I A	2150
1851	GAAGATCCCCCATCTGAAGCCCGCCTTCGCTGACGGTGGCAGGTCACGG -----+-----+-----+-----+-----+ CTTCTAGGGGTAGACTTCGGGCGGAAGCACTGCCACCGTGCCAGTGCC K I P H L K P A F R D G G T V T A	1900	2151	GATGAAGGAGCTTGGCCCTGCACAGATGCACGAACATCAACGGCGGGG -----+-----+-----+-----+-----+ CTACTTCTCGAACCAGGAGGTGTCTACGGTGTCTGTAGTTGCCGCCGCC M K E L G L P H D A T N I N G G A	2200
1901	CGGCGAACAGCTCGTCGATCTCGGACGGGCGCGCGGCTGGTGATGATG -----+-----+-----+-----+-----+ GCCGCTTGTGAGCAGCTAGAGCTGCCCGCGCGCGGACCACTACTAC A N S S S I S D G A A A L V M M	1950	2201	CCTGCCGCTTGGGCATCCCATCGGCGCGTCCGGGGCGCGGATCATGGTC -----+-----+-----+-----+-----+ GGACGGCGGAACCCGTAGGTAGTACCGGCGCAGCCCCCGCGCTAGTACCAG C A L G H P I G A S G A R I M V	2250
1951	CGCCAGTCGAGGCGGAGAGCTGGGCTGACGCCGATCGCGCGGATCAT -----+-----+-----+-----+-----+ GCGGTACGCTCCGGCTCTTCGACCCGACTGGCGCTAGCGCGCTAGTA R Q S Q A E K L G L T P I A R I I	2000	2251	ACGCTGTGAACCGGATGCGCGCGGGCGCGACGCGCGGGCGCGCATC -----+-----+-----+-----+-----+ TCCGACGACTTGGCTACCGCGCGCGCCCCCGCGCTGCGCGCCCCGGCGTAG T L L N A M A A R G A T R G A A S	2300
2001	CGGTGATGCGACCCCATGCCGACGTCGCCGCGCTGTTCCGACGGCCCCCA -----+-----+-----+-----+-----+ GCCAGTACGCTGGGTAGGCTGGCAGGCGCGGACAGGCTGCCGGGGGT G H A T H A D R P G L F P T A P I	2050	2301	CGTCTGCATCGCGGGGGCGAGGCGACGGCCATCGCGCTGAACGGCTGA -----+-----+-----+-----+-----+ GCAGACGTAGCGCCCCCGCTCCGCTGCCGTAGCGCGACCTTGCCGACT V C I G G G E A T A I A L E R L S	2350
2051	TCCGCGCGATCGCGCAGCTGTGGACCGCACGGACACCCGCCCTTGGCGAT -----+-----+-----+-----+-----+ AGCCGCGCTACGCGTTGACGACCTGGCGTGCCGTGGGCGGAACCGCTA G A M R K L L D R T D T R L G D	2100	2351	GCTAATTCATTTTGGCGGAAATCCGCGTTCGTCGACGATGGGGGAACCG -----+-----+-----+-----+-----+ CGATTAGTAACGCGCTTAGCGGCAAAAGCACGTGCTACCCCTTGGC *	2400

**FIG. 7D**

2401	GAAAGGCCAGCCCTGTTGTTGGTTCGATCGACCTGTCTTTCGGGCCATGCC -----+-----+-----+-----+-----+ CTTTTCCGGTCCGGAACAACACACGACGCTGGACAGAGCCCGGTACGG	2450	2701	2750	GTCTGCGATGCGATGGTTCGATGCGCGCTGCGGTGAGATGGTCCATGC -----+-----+-----+-----+-----+ CAGACGCTACGCTACGACTACGGGACGGCGACGCTCTTACCGGTACG  V C D A M V D A A C A V E M V H A
2451	CGTAGCCGATGTGGCAGGCGCATGGGGCGTTTCCGATCCTGGTCCCATGA -----+-----+-----+-----+-----+ GCACTGCGCTACACCTCCGCTACCCCGCAACGGCTAGGCCAGGTACT	2500	2751	2800	CGCATCGCTGATCTTCGACGACATGCCCTGATGAGCATGCCAGGACCC -----+-----+-----+-----+-----+ GCGTAGCGACTAGAAAGTCTGTACGGGACGTACTGCTACGGTCTCTGGG  A S L I F D D M P C M D D A R T R
2501	CTGACGCCAACGAAGGACCGATGACGCCCAAGCAGCAATCCCCCTACGC -----+-----+-----+-----+-----+ GACTCGGTTGCTTCCTCGGTACTGCGGGTTCTGCTTAAGGGGATCGG  crrE --> M T P K Q Q F P L R	2550	2801	2850	GTCGCGGTCAAGCCCGCCACCCATGTGCGCCATGGCGAGGGCGCGCGGTG -----+-----+-----+-----+-----+ CAGCCGACAGTCGGGGCGGTGGGTACAGCGGTACCGCTCCCGCGCGCCAC  R G Q P A T H V A H G E G R A V
2551	GATCTGGTCGAGATCAGGCTGGCGCAGATCTCGGGCCAGTTTCGGCGTGGT -----+-----+-----+-----+-----+ CTAGACCAGCTCTAGTCCGACCGCGTCTAGAGCCGGTCAAGCCCGCACCA  D L V E I R L A Q I S G Q F G V V	2600	2851	2900	CTTGGCGGCATCGCCCTGATCACCGAGGCCATGCGGATTTTGGGCGAGGC -----+-----+-----+-----+-----+ GAACGCCGCTAGCGGACTAGTGGCTCCGTTACGCTAAACCCGCTCCG  L A G I A L I T E A M R I L G E A
2601	CTCGGCCCCGCTCGGGCGCGCCATGAGCGATGCCGCCCTGTTCCCCCGGCA -----+-----+-----+-----+-----+ GAGCCGGGCGAGCCGCCGCTACTCGCTACGGCGGACAGGGGCGGT  S A P L G A A M S D A A L S P G K	2650	2901	2950	GCGCGCGCGACGCCGGATCAGCGCGCAAGCTGTGTCATCCATGTGCGC -----+-----+-----+-----+-----+ CGCGCGCGCTGCGGCCCTAGTCCGCGCTTCGACCGAGGTAGGTACAGCG  R G A T P D Q R A R L V A S M S R
2651	AACGCTTTCGCCCGTGTGATGATGATGCGCGCAAGCTCGGGCGGG -----+-----+-----+-----+-----+ TTGCGAAGCGCGGACGACTACGACTACAGCGGCTTTCAGGCCCGCCC  R F R A V L M L M V A E S S G G	2700	2951	3000	GCGCGATGGACCGGTGGGCTGTGCGCAGGCGAGGATCTGGACCTGCAC -----+-----+-----+-----+-----+ CGCGTACCTGCGCCACCCGACAGCGGTCCGTCCTAGACCTGGACGTG  A M G P V G L C A G Q D L D L H

FIG. 7E

		Applicant(s):	Luis PASAMONTES and Yuri TSYGANKOV
		Parent Serial No.:	09/920,923
		For:	<b>FERMENTATIVE CAROTENOID PRODUCTION</b>
3001	3050	3301	3350
G C C C C C A A G G A C C C C G C G G A T C G A A C G T G A A C A G G A C C T C A A G A C C G G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C G G G G T T C C T C G G C G C C C T A G C T T G C A C T T G C A C T T G C T G G A G T T C T G G C C A P K D A A G I E R E Q D L K T G			A G C C G C G C G C A A C T G G A C G A G C T G A T G C G C A C C C G G C T G T T C C G C G G G G G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ T C G G C G C G C G T T G A C C T G C T C G A C T A C G C G T G G C C G A C A A G G C G C C C C C S R A Q L D E L M R T R L F R G G
3051	3100	3351	3400
C G T G C T F T C G T C G C G G C C T C G A G A T G C T G T C C A T T A T T A A G G T G T G G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ G C A C G A C A A G C A G C C C G G A G C T C T A C G A C A G G T A A T A T T C C C A G A C C V L F V A G L E M L S I I K G L D			G C A G A T C G C G G A C C T G T G C C C C G T G C T G C C G C A T G A C A T C C G C C G C A -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C G T C T A C G C C T G G A C G A C C G G G C G C A C G A C G G C G T A C T G T A G G C G G C G T Q I A D L L A R V L P H D I R R S
3101	3150	3401	3450
A C A A G C C G A G A C C G A G C A G C T C A T G G C C T T C G G G C G T C A G T T G T G C G G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ T G T T C C G C T C T G G C T C G T C G A T A C C G G A A C C C C A G T C G A A C C A G C C K A E T E Q L M A F G R Q L G R			G C G C T A G G C G C G G T C G G T C C A C A G G C G T C G C G G C T G A T T T C G C C G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C G C G A T C C G C G C C A G C C C A G G T G T C C G C A G C C C G A C T A A A G C G C A * A R P R T W L G D R S I E G
3151	3200	3451	3500
G T C T T C C A G T C C T A T A C A C C T C G T G G A C G T G A T C G G C G A C A A G G C C A G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C A G A A G T C A G G A T A C T G T G G A C G A C C T G C A C T A G C C G C T G T T C C G G T C V F Q S Y D D L L D V I G D K A S			C C G C G A G G C G C A T C G G C C G C C T C C A A G C C T C C G C G C G C C A G A A G C C C -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ G C G C G T C C G C G T A C G C C G C G C A G G T T C G G A G G C G C G G T C T T C G G G G R L R S A A A D L G G R A L L G
3201	3250	3501	3550
C A C C G G C A A G G A T A C G G C G C G A C C G C C C C C C C C G C C C A A A G G G C G -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ G T G G C C G T T C C T A T G C C G C G C T G T G C G C G C G G G C C G G G T T C C C G C T G K D T A R D T A A P G P K G G			G A T C T T G C A G C C T T C G A C G T G C T G A T C C G C T G C G A T A G G C C T C G G G C -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C T A G A C C G T C G G A A G C T G C A C G A C T A G G C A C C G C T A T C C G A G C C C C G I K A A K S T S I R Q R Y A E P
3251	3300	3551	3600
G C C T G A T G C G T C G G A C A G A T G G C G A C G T G G C G C A G C A T T A C C G C C C -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ C G G A C T A C C G C C A C C T G T C T A C C G C T G A C C G C C T C G T A T G G C G C G G L M A V G Q M G D V A Q H Y R A			C A C C C T C C C G A T G C G C T C C G A T T C G C A T T A G A T A C G A C A G C G C G G C -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ G T G G A C G G C C T A C G C G A G G G T A A C G C G T A T C T A T G C T G C G C G C G C G G Q R I R T G I A R Y I R L A A

**FIG. 7F**

3601	CGGATCGACACGCGCAGCGCGCGGCGAGATGCGGAACCCCTCGCGCGC -----+-----+-----+-----+ CGCTAGCTGTGCGCGTCGCGCGCGCTTACGCCCTTCGGGAGCGGCGG	3650	3901	CCGACGACCCCGCGACGTGGTAGGAATATCCAGCACGTATCCAGGCT -----+-----+-----+-----+ GGGTGCTGGGGCGCTGCACCATCCTTATAGGTCGTGCAGTAGGTCCGA	3950
	A I S W A C R P P L H P L G Q R A			G V V G A V H Y S Y E L V D D L S	
3651	CGAGGCATAATAGGGCTCGGCGCGCTCAAGCAGCGGATGATGACGGAAT -----+-----+-----+-----+ GCTCCGTATTATCCCGAGCGCGGCGAGTTCTGTCGCCCTACTATGCTTA	3700	3951	GGCGTATTGCGGATCCGCGACATCCATCGCGAAACCTCGATCAGTCCA -----+-----+-----+-----+ CGCCATAAGCGCTAGGCGCTGTAGTAGCGCTTTGGGAGCTAGTCCAGGT	4000
	S A Y Y P E A A D L L R I I V S			R Y E R D A V D M A F G E I L D	
3701	AGAGCGCTCGAAGGACCGGACCCCTCAACCTCGGCCCGCTCGGC -----+-----+-----+-----+ TCTCGCGCAGGCTTCGTGCGCCTGGAGTTGGCAGCGGGGCGGAGCGCG	3750	4001	TCGGCCAAAGTTCGCGGAATCATGCCCGCGGGCGACTGGGCGAGCGCC -----+-----+-----+-----+ AGCGGTTTCCAGGCCCTTTAGTACGGCGGCCCGCTGGACCGCGTCGCGG	4050
	Y L A D S P V P G E V T A G A E A			M P W L D P F D H R R A V Q R L A	
3751	AGCCAGTCGGAGGCAGATAGCAGCGCCCGATGCGCGGATCTGTCGATCA -----+-----+-----+-----+ TCGGTCAGCCGTCGCTTATCTGTCGGGCGCTACCGCGGTAGCAGCTAGTG	3800	4051	GCGAAGGGCGGACATCGGGCGCTCTCTGTGCGCGGCGCAGCGGTCT -----+-----+-----+-----+ CGCTTCCCGCGCTGTAGCCCGGCGAGGACAGTCGCGCGCGGTGCGACAG	4100
	L W D A P L Y C R G I A A D D I V			A F P P S M P G D E H L A A L T D	
3801	GTCCGAGCGATGTTCTCAGCTGGAACGCAAGGCCAGATCGCAGGCGC -----+-----+-----+-----+ CAGCGCTCGTACAGCAGTCGACCTTGGGTTCCGGGTCTAGCGTCCGCG	3850	4101	GGCGCGCAGCGCCCCCAGCGCGCTGTGGGTGCGCGCCCGCTCGGGGG -----+-----+-----+-----+ CCGGCGCTCGGGGGGTGCGCGCGGACACCCAGCGGCGGCGAGCCCCC	4150
	D R A I N T L Q F A L G L D C A			A R L A G L R A Q P D G G A E P	
3851	GATCCAGCACCCATCTCTCTGCAGCGCCCATCACCGCGGCCATCATCAG -----+-----+-----+-----+ CTAGGTCGTGGCGTAGCAGGACGTGCGGGTAGTGGGCGCGGTAGTAGTC	3900	4151	CAGAACCCATCACCTGCCCGTTCGATCAGCTATCCGATGCTGACCCAG -----+-----+-----+-----+ GTCTTGGGTAGTGACGCGGCGAGCTAGTCAGTAGGCGTACGGACGTGTC	4200

R D L V A D D Q V G M V R A M M V

4201	GCATAGAGCATGACCGGTATCTCTCGCGGATGCCGGCGGCATCAGCTTGGC -----+-----+-----+-----+-----+ CGTATCTGTAAGGATAGGAGCGCTACGGCCGCGGTAGTCGAACCG	4250	4501	4550	CGTGATGGGCGGACAGTTCCGTCTGCTGAAATCGGCGGGGCTGAAGATCGCG -----+-----+-----+-----+-----+ GCACTACCCGCTGTCAAGCCACGACTTTAGCGCCCCGACTTCTACGCC G H A S L E T S F D A P S F I R
4251	A Y L M V T D E R I G P P M L K A CGCTCGCGGAGCTTTGGCAACCTGCGCGATGGCCGCTTCGGAGTCG -----+-----+-----+-----+-----+ GCGAGCGCTTCGAACGCTTGGACCGGCTACCGGCGGAAGCCTTACG	4300	4551	4600	CTGACGGTCAAGTCTTGGCAGGTCCGGGATGGCGCGGCGCTCCAGTTT -----+-----+-----+-----+-----+ GACTGCCAGTCCACGAACGGCTCCAGCCCTACCGGCGCGGAGGTCAAG S V T L H K R L D P I A R R E L E
4301	A Q A F S Q S G Q A I A A E S T CCGTGAGATCGTATCGGACCGCCAGTCCGACAGCATGACCTGGCGG -----+-----+-----+-----+-----+ GGCAGTCTAGCCAGTACCTGCCGCTCCAGGCTTCGTACTGGACCGGG	4350	4601	4700	CTCGAAGATCGCTCGGCATAGCCCCGGGGCTTCGGCTTCCCAATCGACAT -----+-----+-----+-----+-----+ GAGCTTCTACCGGAGCGGTATCGGGCCCCGGAGCCGAAGGTTAGCTGTA E F I R E A Y G P A E A E W D V
4351	A T L D T M <--- crtB TGGCTTGGCTGCCAACGACACCGGGATGCCCGGCACCGCGGATCGGTG -----+-----+-----+-----+-----+ ACCGAACCGGACGCTGCTGTGGCCCTACGGCGTGGGCGCTACGCAC T A K A S G V V G P I G A G P H T	4400	4651	4750	CGGCGGGCCAGATGCGGGAACGGGCGCAAGACGTAATCGGTGGACATC -----+-----+-----+-----+-----+ GCCGCGCGGGTCTACCCCTTGGCGGCTTCCTGCATTAACGACCTGTAG D A R G L H P V P A L V Y H T S M
4401	CCCGCCCCACGATGTAGAAGTTTGGGATCGCGGTCGCGGTATGCGG -----+-----+-----+-----+-----+ GGCGGGGTGCTACATCTTCAAGCCCTAGCGGCGCACCGCAATAGCC G A G V I Y F N P I A R D R N H P	4450	4701	4800	CCCTCGGGGCGCAGGCTGGGATCGGTACGCGAGGCGAAATGCAGATACAT -----+-----+-----+-----+-----+ GGAGCCCCCGTCCGACCCCTAGCAGTGGTCCCGCTTACGTCTATGTA G E P A L S P D T V C P S H L Y M
4451	GCGGAACGAGCGGATTGCGTCAAGATCGCTCGACCGAGAGGCGGTGC -----+-----+-----+-----+-----+ CGCCTTGGTCCGCTAACGCAGTCTAGCCGAGCTGGCTCTTCCGCGACG R F W A S Q T L I P E V S F A S	4500	4751		CGAGAAATCGTCCGGCAGGCGTGCCCGGTGAAGATCTCGTTCACGAGCC -----+-----+-----+-----+-----+ GCTCTTTAGCAGGCGTCCGCACCGGGCACTTTAGAGCAAGTGGTCCGG S F D D P L R P G N F I E N V L

FIG. 7H



Luis PASAMONTES and Yuri TSYGANKOV  
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**FERMENTATIVE CAROTENOID  
PRODUCTION**

5401	GATAGACCTCTCTCGCGGTAATCGTGGAAAGCGGGCGATAGCCATCGACATCG -----+-----+-----+-----+-----+ CTATCTGGAGGAGCGCGCAITTAGACACTTCGCGCGCTATCGGTAGCTGTAGC	5450	5701	GGGCTTCGACGATGTTGGTCTCGGATGCGGCGCGATTCGACGGCGATGGCA -----+-----+-----+-----+-----+ CCCGAGAGCTGTATCCACACGAGCGCTACGGCCGGCTAACGTCCGCGCTACCGT	5750
	R Y V E E A Y D H F R R R Y G D V D			R A E V I T T A I G A S Q L R I A	
5451	GCGGATTGAAGAGCGGACCTGCGGGATCAGCTCGTCTGCTGTTTCAC -----+-----+-----+-----+-----+ CGCCCTAATCTCTCGCTCGACCGCCTAGTCGAGCAGCAGCAAGTG	5500	5751	AGCGCAAGCCCGCCGAAACCTGCGCGCGATGACGATGGCGGAACTCATGCT -----+-----+-----+-----+-----+ TCGCGTTGCGGGCGCTTTGGACGCGGTACTGCTACCGCCTTGAGTACGA	5800
	A P N F S A V Q R I L E D D N V			L A L G G F G A G I V I A S S M <-- crtI * A	
5501	GTATTGGAAGCTGCGGCGCTCCGCCCATGTTCAGCCGGTAGAAGGGCGAGA -----+-----+-----+-----+-----+ CATAGCTTCGACCGCGGAGCGGGGTACGTGCGGCATCTTCCCGCTCT	5550	5801	CTCTCTGCACAGGGGGCGTTCCGGGAGGACGCGACGCGCTTCGACAG -----+-----+-----+-----+-----+ GAGAGGAGCTGCTCCCGCGCAAGCCCGTCCGTCGCGTGCCGCGGACGCTGTC	5850
	Y E F S R G D A W T L R Y F P S			R E Q L L P R E P L C R V A Q S L	
5551	CCGGCAGCAGCGTCAGTCAAGCTCCATCGGTTGGCGCTGAGGGCCAC -----+-----+-----+-----+-----+ GGCGTCTGTCAGTGCAGTCGAGGAGTAGCCAAACCGGCGACTCCCGGGTG	5600	5851	CGGAATGGGCGGGCGTCCGGTGACGATGCGGAAGCCGGTGGCCCAATGTCA -----+-----+-----+-----+-----+ GCCTTACCGCGCGCAGGCCACTGCTAGCTTCGGCCAGCCGGTTACAGT	5900
	V P L L T V D R E M P Q G S L A W			P I P P R G T V I R L R D A L T	
5601	AGCTCTCGCAGCGTCTCGGGTCTGGTCACGACCGTCCGGGCTGTCATCGAA -----+-----+-----+-----+-----+ TCGAGAGCGTCCGACAGCCCGACCGACGCTGTCGCGAGCCCGGACGTAGCTT	5650	5901	GGCGCCCGGCATAGAAAGCGCTCGATCAGCGGCTCGGGCAGCGGGTAGAAC -----+-----+-----+-----+-----+ CCGCGGCGCGTATCTTCGCGAGCTAGTCGCCCGCAGCGCGCTCCGCCATCTTG	5950
	L E R L S D P D T V V T P G A D F			L R G A Y F R E I L P Q P L R Y F	
5651	GACGTGGCCCTGATCGTTCCACACATAGGCGCGGCCCGGGCTTGTGCG -----+-----+-----+-----+-----+ CTGCACCGGACTAGCAAGTCTGTATCCGCGCGCGCGGCCCGCAACAGCG	5700	5951	CGCTGCACAGGCGATAGCAGCGTTCGGGCGGGCAGCCCGGAACAGCAT -----+-----+-----+-----+-----+ GGCAGCTGCTCCGCTATCGCTGCAGCGCCCGCGCTCGGCGCCTTTCGTA	6000
	V H G Q D N W V Y A R G G P K D			R Q L L R Y R R D P P C G R F L M	

FIG. 7J



6001	CCGGTTGAGCAGCCGAGGAAGCGGTGCGGATCCGCGCGGATCGATGCCCC -----+-----+-----+-----+-----+ GGCCAACTGTCGGCGCTCTTCGCCAGCGGTAGCGCGCTAGCTACGGGG	6050	6301	CAGCGAGCCCTGCGCCAGCGCGCATCGTCCAGATCGCCGCCGTCGTGT -----+-----+-----+-----+-----+ GTGCTGCGGAGCGCGGTGCGCGTAGCAGGTCTAGCGGCGCAGCGACA	6350
6051	R N L L P L F R D R D A R D I A -----+-----+-----+-----+-----+ AGCCGCGCAACCGCGGACGGGCGGACCGGTCCTCAGGTCCGCGCGCGG -----+-----+-----+-----+-----+ TCGGCGGTGGCGCGCTGCCCGCTGCGCGCAGAGTCCAGCGCGCGCGC	6100	6351	AGCGGTATCTCTGATCAGGATCGGGTGGACTGAAGGCGAGCAGATAG -----+-----+-----+-----+-----+ TCGGCGATAGGAGCTAGTCTACGCCACCCTGACTTCCGTCGTCTATC	6400
6101	W G R V A R R A S A T T L D R A A -----+-----+-----+-----+-----+ ATGGCATCCGACCTGCGCGGCATAGGCGAGCGAATATCCGGTGAGGG -----+-----+-----+-----+-----+ TACCGTAGCGGTGGACGCGCGGTATCCGTCGCTTATAGCCACTGCCC	6150	6401	ATGAAGCGGTACCCGTCCAATCTCGGGAACGGTCGCGTCATGATCATCGG -----+-----+-----+-----+-----+ TACTCGCCATGGGCGAGTAGACGCCCTTCCAGCGCAGGTACTAGTACC	6450
6151	I A D A V Q A A Y P L S Y G T V P -----+-----+-----+-----+-----+ GTGGAACAGCCTGCCCCAGCCCAACCGGACCCGCCCTGCGCGTGGT -----+-----+-----+-----+-----+ CACCTTGCGGACGGGGTTCGGTTGCGGTGCGGGGAGCGGCACCA	6200	6451	GCGTTCGACGCCATGGGGGCGTCGGTCTCGATCTCGACGCCACCGAAT -----+-----+-----+-----+-----+ CGCGAGCTGCGGTACCCGCCGAGCCAGAGCTAGAGCTCGGGGTCTTAA	6500
6201	H F L G A G L G V P V A G Q A H -----+-----+-----+-----+-----+ CGCGCAGAGCCTATGCGGTATGGGCCAGCGCATGGGAGGATGCCC -----+-----+-----+-----+-----+ GCGCGTCTTCGGATACCGCAGTACCGGTGCGGTACCCGTCCTACGGG	6250	6501	TCTGGAACCCACGCTCAGGTGCGGGGTCTCGACGGCACACGGGCGTCG -----+-----+-----+-----+-----+ AGACCTTGGGTGCCAGTCCACGCCGCCAGAGCTGCCGTGTCGCCGAGC	6550
6251	D R W F G I A D H A L A I P L I G -----+-----+-----+-----+-----+ CTTTCGCGCGCATCTCTGTCGCGGTCCAGCCCCCGCTGGCGGATAGTC -----+-----+-----+-----+-----+ GAAAGCGCGCTAGAGACGGCCAGGTGCGGGGCGGACCGCCGTATCAG	6300	6551	ATCAGCAGGCGAGCTCGATCCGCGAGCGCTCCGTCCGTCCGTCGCGCGGT -----+-----+-----+-----+-----+ TAGTGGTCCGTCCGAGTAGCGCTCGGCAGGAGTCCGAGCGCGGCCCA	6600

FIG. 7K

I V C A A E I R S G D T L T A G T

6601	ATCGTCCAGCGCTCGGCACATGCGGTATTCCACCCGAGATGACACCCCTGCATAGCAGGTCCGACGGCTGTACGCATAGGTGGCGTCTAGCTGTGGGACGT	6650	ACCGGACAGCCCGCGCGCCGATCAGCAGATCATGGCTCATGTATTGGCTGGCCCTGTTCGGGGCGCGGGCGCTAGTCTAGTACCGAGTACATAAGCG	6901	G S L G A G A I L L D H S M ←-- crty	6950	ACCGGACAGCCCGCGCGCCGATCAGCAGATCATGGCTCATGTATTGGCTGGCCCTGTTCGGGGCGCGGGCGCTAGTCTAGTACCGAGTACATAAGCG
6651	GCAGCCCGATCAGCGCGCCCGCTCGATCGAGCCATAGCCTGTCTGCTCAGGCGTCCGGCTACTCGCGGGCGGAGTAGCTCGGTATCGGACAGCAGTCC	6700	ATCCGCCCCCTTCGCGGTCTTCAGCAGCGGCGCCGAGCGTTTCAGCTCTGTATCCGGGGAACGCCCAAGTCTCGTCGGCGGGCTCGCAAGTCTGAGAC	6951	D A G E R D K L L A G S R K L E	7000	ATCCGCCCCCTTCGCGGTCTTCAGCAGCGGCGCCGAGCGTTTCAGCTCTGTATCCGGGGAACGCCCAAGTCTCGTCGGCGGGCTCGCAAGTCTGAGAC
6701	CGGCGCGAATGGTCGGGAAACCGGACCTCTGATCCGTCCTATTCCCGCGCGCGCTTACCGCCCTTCGCGCTGAGGACTAGGCGAGTAAGCGGCGC	6750	CCTTGAGGCTGTCCAGCCGAGGGCGCCAGATGAACCAAGCTGACGACGGAACTCCGACGTGGCTCCCGGGGTCTACTTTTGGCTTCGACTCGGCTC	7001	A K L S D V S P A W I F G F S V C	7050	CCTTGAGGCTGTCCAGCCGAGGGCGCCAGATGAACCAAGCTGACGACGGAACTCCGACGTGGCTCCCGGGGTCTACTTTTGGCTTCGACTCGGCTC
6751	ACGAATGGGCGACAGCGCGCCGAGCCATTGCGGGAAGATCCGTGTGTTGCTTACCCGCTGTCCGCGCGTTCGTAAGCCCGCTTCTAGGCACAGCA	6800	TTCTCCGGGCGATGACCGGCGTATGCATCTCTGTGTCTGTTAGTAGCGGTAAGAGCCGGTACCTGCGGCACTACGTAGGACACACGGACCATCTCGGCNERGHVAHHMRHAQYVR	7051	TTCTCCGGGCGATGACCGGCGTATGCATCTCTGTGTCTGTTAGTAGCGGTAAGAGCCGGTACCTGCGGCACTACGTAGGACACACGGACCATCTCGGCNERGHVAHHMRHAQYVR	7100	TTCTCCGGGCGATGACCGGCGTATGCATCTCTGTGTCTGTTAGTAGCGGTAAGAGCCGGTACCTGCGGCACTACGTAGGACACACGGACCATCTCGGCNERGHVAHHMRHAQYVR
6801	GGCAGGACCAAGGTGTCTGTTCCGAGGGGCGGACCGCGGCTCGAGCATCCGTTCTTGTTCCACAGCACAGGCTCCCGGCTCGCGGCGCAGCTCGTAG	6850	ACGAACATAGCCCGCGCTTGGGGACATAGCGGAACGGCCAGCGCCCATGCAATGCTTCTATCGCGCGGAACCCCTGTATCGCCTTGCCTGCGGTCGCGGTTAGTRLYGGRKPPVYRFPWRGH	7101	ACGAACATAGCCCGCGCTTGGGGACATAGCGGAACGGCCAGCGCCCATGCAATGCTTCTATCGCGCGGAACCCCTGTATCGCCTTGCCTGCGGTCGCGGTTAGTRLYGGRKPPVYRFPWRGH	7150	ACGAACATAGCCCGCGCTTGGGGACATAGCGGAACGGCCAGCGCCCATGCAATGCTTCTATCGCGCGGAACCCCTGTATCGCCTTGCCTGCGGTCGCGGTTAGTRLYGGRKPPVYRFPWRGH
6851	ACGATCGCGCATCCGGTCTGCGGTTCGGACGCAACGCAAGCGCGATCAGCGCTAGCAGCGGTAGGCAGACCGCACGCGCTTGCCTTCGCGCTAGTCGGVIRADPPRRDRVA LA I L A	6900	CCAAGCCGTATGCAGGAAATAGTAGATGACCCCTAGCAGGTGACCCCCGGTTCGGCAGTAGCTCCTTTATCATCTAGTCGGGCATCGTCCACTGGGGV L G D H L F Y Y I L G Y C T V G	7151	CCAAGCCGTATGCAGGAAATAGTAGATGACCCCTAGCAGGTGACCCCCGGTTCGGCAGTAGCTCCTTTATCATCTAGTCGGGCATCGTCCACTGGGGV L G D H L F Y Y I L G Y C T V G	7200	CCAAGCCGTATGCAGGAAATAGTAGATGACCCCTAGCAGGTGACCCCCGGTTCGGCAGTAGCTCCTTTATCATCTAGTCGGGCATCGTCCACTGGGGV L G D H L F Y Y I L G Y C T V G

FIG. 7L

7201	ACCGCAGCCACCAGGCCAGATCCGACCCCATCGCGCCGATCGCGAACAG -----+-----+-----+-----+-----+ TGGCGTCCGTGGTCCGGTCTAGGCTGGGTAGCGCGGTAGCGTTGTC V A L W W A L D S G M A G I A F L	7250	ATGACCAGCCCATCGGGGTGCGACCAAGGGCATCGCGTGACATCTCGGT -----+-----+-----+-----+-----+ TACTGGTGGGTAGCCCCACGCTGGTTTCCCGTAGCGCACTGTAGACGA	7501	7550
7251	CACGATCGAGATTACCGCGAGAGATGACGCCATAGAGGTGTTCTTCTCGA -----+-----+-----+-----+-----+ GTGCTAGCTCTAATGGCGCTTCTACTGGGTATCTCCAGCAAGAGAGCT V I S I V A F I V G Y L D N K E	7300	TCAGGGCTCATAGCGGATCATCCGTGACATTCGCCGCCGACGCGGAG -----+-----+-----+-----+-----+ AGTCCCGAGTATCCGCCCTAGTAGGCACTGTAAAGCGGGGCTTGGCCGCTC	7551	7600
7301	GCGGTGGTCGTGATCCTCGTGGTGGTGCATTTATGCCAGCCCCAGCCC -----+-----+-----+-----+-----+ CGGCACCAAGACTAGGAGCAGCACCGCTAAATACGTCGGGTGCGG L A H D H D E D H H S K H W G W G	7350	GCGCATCAGCGCTCCGTCGCTGGAAATAATATGTTTCCGAAGATGG -----+-----+-----+-----+-----+ CGCGTAGTCGCAAGGACGACCTTTATAATTACAAAAGGGCTTCTACC	7601	7650
7351	AGGGGGCAATGCATCCACCGATGGACGGAGTAGGCCGTCACTCCAT -----+-----+-----+-----+-----+ TCCCCGGTACGTACTAGGTGGCTACCTGCCTCATCCGGCAGTCGAGTA L P G H M I W R H V S Y A T L E M	7400	TCGGGGGAGAGGATTGCAACCTCCGACCTACGGTACCCAAAACCGTCGC -----+-----+-----+-----+-----+ AGCCCCGCTCTCCTAAGCTTGGAGGCTGGATGCCATGGGTTTTGGCAGCG	7651	7700
7401	CGCGGCGACGTCAGGATGACGGTCAGGATTCGGGGCCCAAGTGTCTATGC -----+-----+-----+-----+-----+ GCGCGCTGCCAGTCTACTGCGAGTCTTAACGCCGGGTTACAGTAGC A A V T L I V T L I A A W T S M <--- crtZ	7450	GCTACCAGGCTGCGGTACGCTCCCGACTCGCGGAAGCTTTAGCCGATTGT -----+-----+-----+-----+-----+ CGATGCTCCGACGGGATCGGGGCTGACGCTTCGGAATCGGGTAACAA	7701	7750
7451	CGCCCCCTTGCTTATATGACGGGAACAGGTACGCTGCCGCGCGGTGC -----+-----+-----+-----+-----+ GCCGGGGAACGAATATATCTGTCCCTTGTCCGATGCCACGGCGGCCACG	7500	CCGGCAAGGGAAAGACCTAGTCCAGGCCAGGCCATTTGTCGCCCATG -----+-----+-----+-----+-----+ GGCGGTTCCCTTTCTGGATCAGGTCGGTCCGTCTCGGTAAACAGCGGTAC	7751	7800

FIG. 7M \* D C A L V A N D G M

7801	CCCGGATGCGCCATCGGCTGACCGGGCTTCAAGGCCAAGGCGATCCGCTC -----+-----+-----+ GGGCTACCGGTAGCCGACTGGCCGGAAGTCCGGTTCCGCTAGGGCGAG	7850	8101	GGCGGTCTTCGGGGTGTTCGGGCACTCGACCCGAAACCCGAGCGTTTC -----+-----+-----+ CGCGCAGAAAGCCCGACAGGCGTGGAGCTGGGCTTTGGGCTCGCAAG	8150
7851	G P H A M P Q G P K L G L R D A E TCCGCCCCGATTTTCAGAGGAGCAAGCCGGTCCGGTCCGGATCGCCGA -----+-----+-----+ AGCGGGCGCTAAAGCTCTGCTTGTGGCCAGCCCCAGGCCCTAGCGGT	7900	8151	CGCACCGGTATCGACGACAAGACTGCCGGGCGCGGATTCCACCGCCGCG -----+-----+-----+ GCGTGCCATAGCTGCTGTTCTGACGGCCCGCGCTAAGTGGCGGCGGC	8200
7901	G G A I E L V F L R D P D G CCGCCGCGCGGATGGGCGTCTCGTCCAGCGGGCGCGCATTTGCGGTG -----+-----+-----+ GGCGGCGGCGCTTACCCGACAGCAGTCCCGCGCGTAAGCCACC	7950	8201	CGCGCGGGGATCAGGACCGCAAGAGCGCTCGGGCTTACTCGGCCAC -----+-----+-----+ GCCGCCCGCTAGTCTCGTGGCGTTCTTCGGGACCGCGGAATGAGCCGCTG	8250
7951	V A A G P I P T E D L P R A N R H ATGTGGGATGACCCGGTTTCATCCGCAAGACCATGTCCAGCGGAT -----+-----+-----+ TACACCGCTACTCGGGCCAAAGTAGGCGTTTCTGGTACAGGTGCCCCTA	8000	8251	ATGGGCAAGATAGACTGCTCGGCGCCGAGATCTCTGCTGACCTCGCAT -----+-----+-----+ TACCGTTCTATCTGACGAGCCCGGCTCTAGGACGACTGGGACGGTA	8300
8001	I H R I V G T E D A F V M D L P I CAGTGTGTGCGCATCCAGAGGACACCGGCTGGGGCGATTCGTAGATGA -----+-----+-----+ GTACACACGCGTAGGTCTTCTGTGGCCGACCCCGCTAAGCATCTACT	8050	8301	CCTCGTTCGCTCATGCAAGCGCAGGTCCCATGCCGCGATCTGCGCGnG -----+-----+-----+ GGAGCAAGCCAGTACGTGCGGTTCCAGGTTACGGGCTAGACGCGGnG	8350
8051	L T N R M W F S V P Q P S E Y I ACAGATTCCGGTCCCGCAGGAGTCTTTCGGGAACAATCAGGCCCTGC -----+-----+-----+ TGTGTAGGCCACGGGCGTCCGTGAGGAACGCTTGTAGTCCGGGAGG	8100	8351	ATCAGCCCGCGGGACCCCTCGACGACGCGGAGGACATCGCTCGCCGAT -----+-----+-----+ TAGTCCGGCGCGCTGGAGCTGTGCGCTCCGTCTAGCGGAGCGGTA	8400

R T G T M <-- orf-16

**FIG. 7N**

F L M G T G A P L E K R F M L G Q

8401	CACGAGGTCGAGAGCCCGGAATGACGGAGGACCTCGATATGGATGAACA -----+-----+-----+-----+-----+ GTGCTCCAGGCTCTTCGGCCTTACTGCTCTGCGAGCTATACCTACTTGT	8450
8451	CGTCTCGGGGTGGCCGAAGATGTTGGCGAACC GGGAAGGGCCCTTGGC -----+-----+-----+-----+-----+ GZAGGAGCCCCACCGGCTTCTACACCGCTTGGCCCTTTTCGGGGAACCG	8500
8501	CTTGTCGAACCACTTGACGCGGGCCGGACGCGGCGGCGAnCGTCCAGATG -----+-----+-----+-----+-----+ GAACAGCTTGTTGAACCTGCGCCCCGGCCTGCGTCGCCGThnGCAGGTTCTAC	8550
8551	CTCGATCACCTCGGCATCCAGATCGGCGATnGGGGGGTGHnGTGCTTT -----+-----+-----+-----+-----+ GAGCTAGTGGAGCCGTAGGTCTAGCCGCTAnCCCCCCACnGnCAGCGAAA	8600
8601	CnnnCGGTTGATCGACAGGACCTC -----+-----+-----+-----+-----+ GnnnGCCAAGCTAGCTGTCCTGGAG	8625

FIG. 70

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MTPKQQFPLR DLVEIRLAQI SGQFGVVSAP LGAAMSDAAL SPGKRFR AVL  
51 MLMVAESSGG VCDAMVDAAC AVEMVHAASL IFDDMPCMDD ARTRRGQPAT  
101 HVAHGEGRAV LAGIALITEA MRILGEARGA TPDQRARLVA SMSRAMGPVG  
151 LCAGQDLDLH APKDAAGIER EQDLKTGVLF VAGLEMLSII KGLDKAETEQ  
201 LMAFGRQLGR VFQSYDDLDD VIGDKASTGK DTARDTAAPG PKGGLMAVGQ  
251 MGDVAQHYRA SRAQLDELMR TRLFRGGQIA DLLARVLPHD IRRSA

**FIG. 8**

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MTDLTATSEA AIAQGSQSFA QAAKLMPPGI REDTVMLYAW CRHADDVIDG  
51 QVMGSAPEAG GDPQARLGAL RADTLAALHE DGPMSPFFAA LRQVARRHDF  
101 PDLWPMDLIE GFAMDVADRE YRSLDDVLEY SYHVAGVVG VMMARVMGVQD  
151 DAVLDRACDL GLAFQLTNIA RDVIDDAAIG RCYLPADWLA EAGATVEGPV  
201 PSDALYSVII RLLDAAEPYY ASARQGLPHL PPRCAWSIAA ALRIYRAIGT  
251 RIRQGGPEAY RQRISTSKAA KIGLLARGGL DAAASRLRGG EISRDGLWTR  
301 PRA

FIG. 9

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MSSAIVIGAG FGGLALAIRL QSAGIATTIV EARDKPGGRA YVWNDQGHVF  
51 DAGPTVVTDP DSLRELWALS GQPMERDVTI LPVSPFYRLT WADGRSFEYV  
101 NDDDELIRQV ASFNPADVDG YRRFHDYAEV VYREGYLKLG TTPFLKLGQM  
151 LNAAPALMRL QAYRSVHSMV ARFIQDPLR QAFSFHTLLV GGNPFSTSSI  
201 YALIHALLRR GGVWFAKGGT NQLVAGMVAL FERLGGTLLL NARVTRIDTE  
251 GDRATGVTLL DGRQLRADTV ASNGDVMHSY RDLLGHTRRG RTKAAILNRQ  
301 RWSMSLFVLH FGLSKRPENL AHHSVIFGPR YKGLVNEIFN GPRLPDDFSM  
351 YLHSPCVTDP SLAPEGMSTH YVLAPVPHLG RADVDWEAEA PGYAERIFEE  
401 LERRAIPDLR KHLTVSRIFS PADFSTELSA HHGSAFSVEP ILTQSAWFRP  
451 HNRDRAIPNF YIVGAGTHPG AGIPGVVGS KATAQVMLSD LAVA

FIG. 10



Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MSHDLLIAGA GLSGALIALA VRDRRPDARI VMLDARSGPS DQHTWSCHDT  
51 DLSPEWLARL SPIRRGEWTD QEVAFPDHSR RLTTGYGSIE AGALIGLLQG  
101 VDLRWNTHTVA TLDDTGATLT DGSRIEAAACV IDARGAVETP HLTVGFAQKFV  
151 GVEIETDAPH GVERPMIMDA TVPQMDGYRF IYLLPFSPTR ILIEDTRYSD  
201 GGDLLDGALA QASLDYAARR GWTGQEMRRE RGILPIALAH DAIGFWRDHA  
251 QGAVPVGLGA GLFHPVTGYS LPYAAQVADA IAARDLTTAS ARRAVRGWAI  
301 DRADRDRLR LLNRMLFRGC PPDRRYRLQ RFYRLPQPLI ERFYAGRLTL  
351 ADRLRIVTGR PPIPLSQAVR CLPERPLLQE RA

FIG. 11

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MSTWAAILTV ILTVAAMELT AYSVHRWIMH GPLGWGWHKS HHDEDHDLAL  
51 EKNDLYGVIF AVISIVLFAI GAMGSDLAWW LAVGVTCYGL IYYFLHDGLV  
101 HGRWPFRYVP KRGYLRVYQ AHRMHHAHVHG RENCVSFGFI WAPSVDSLKA  
151 ELKRSGALLK DREGADRNT

**FIG. 12**

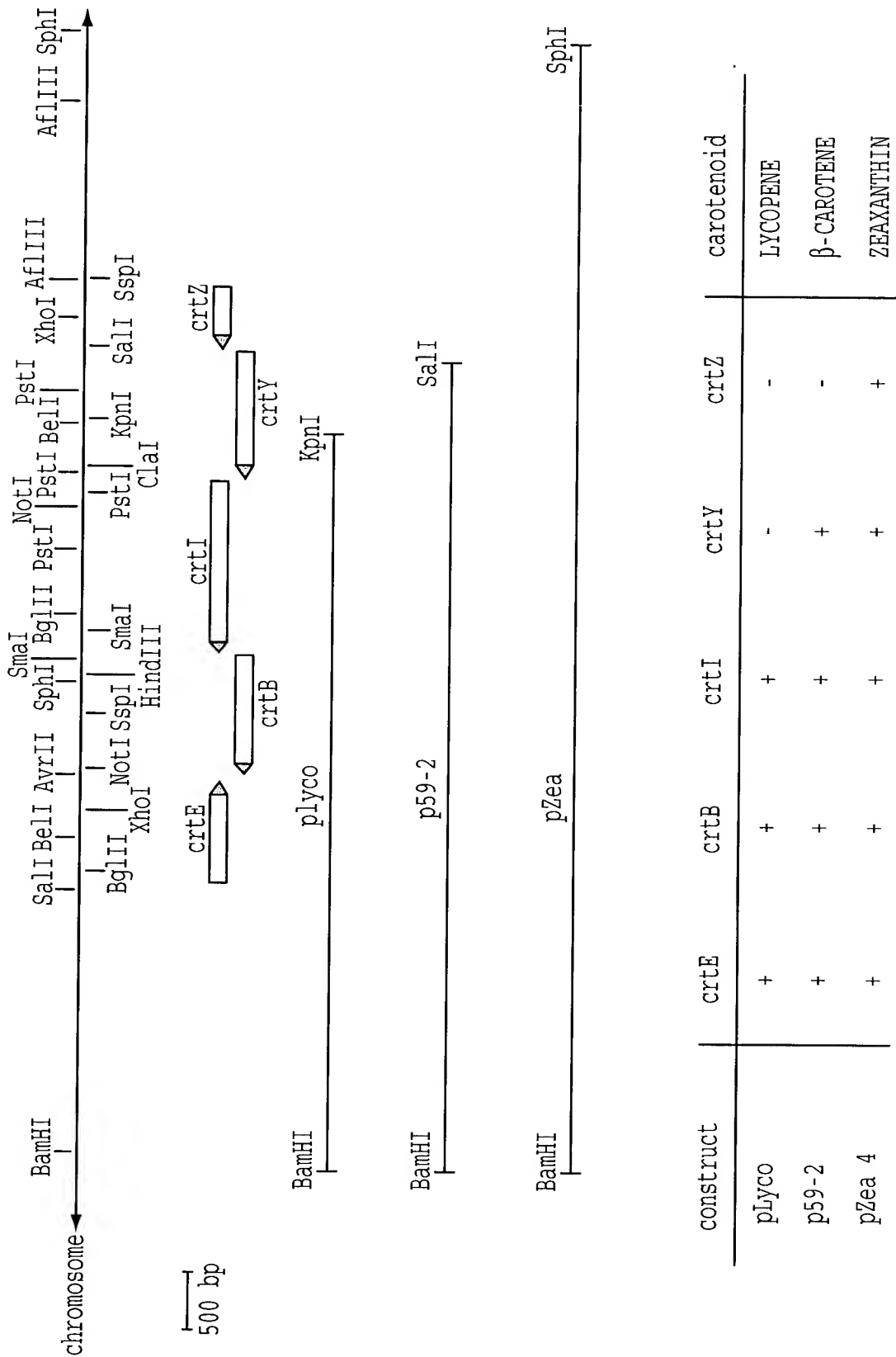


FIG. 13



FIG. 14

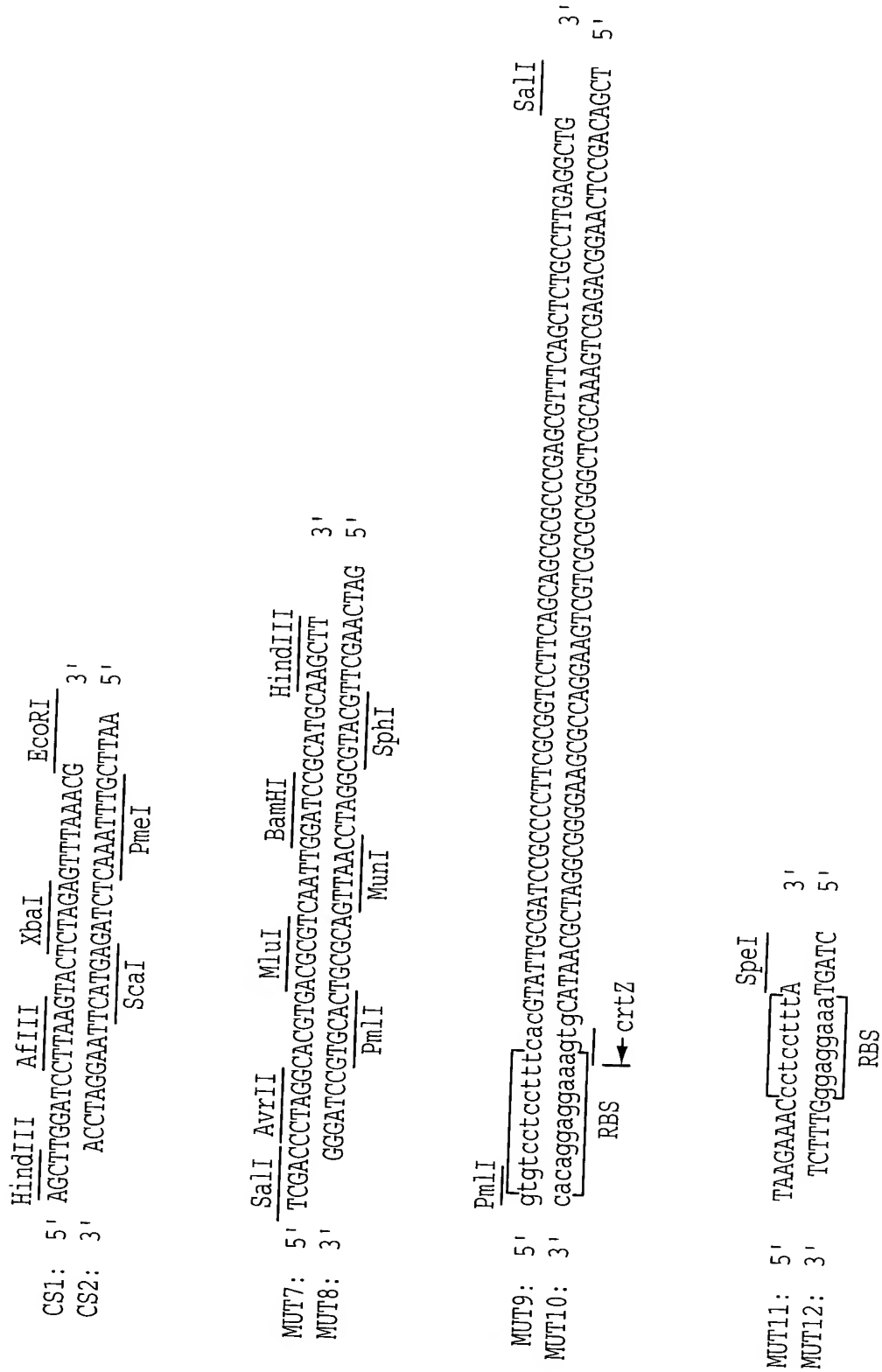


FIG. 15

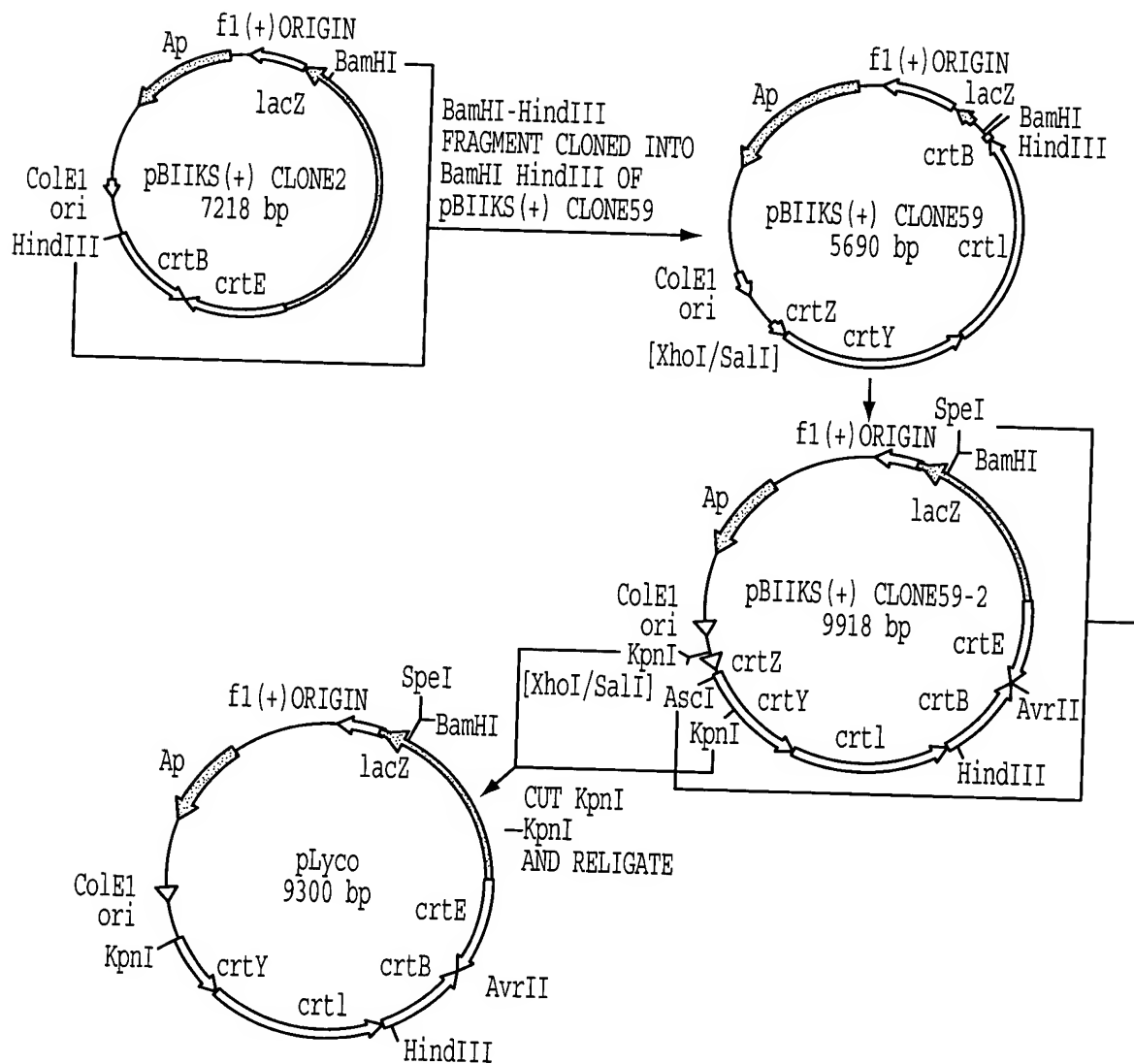
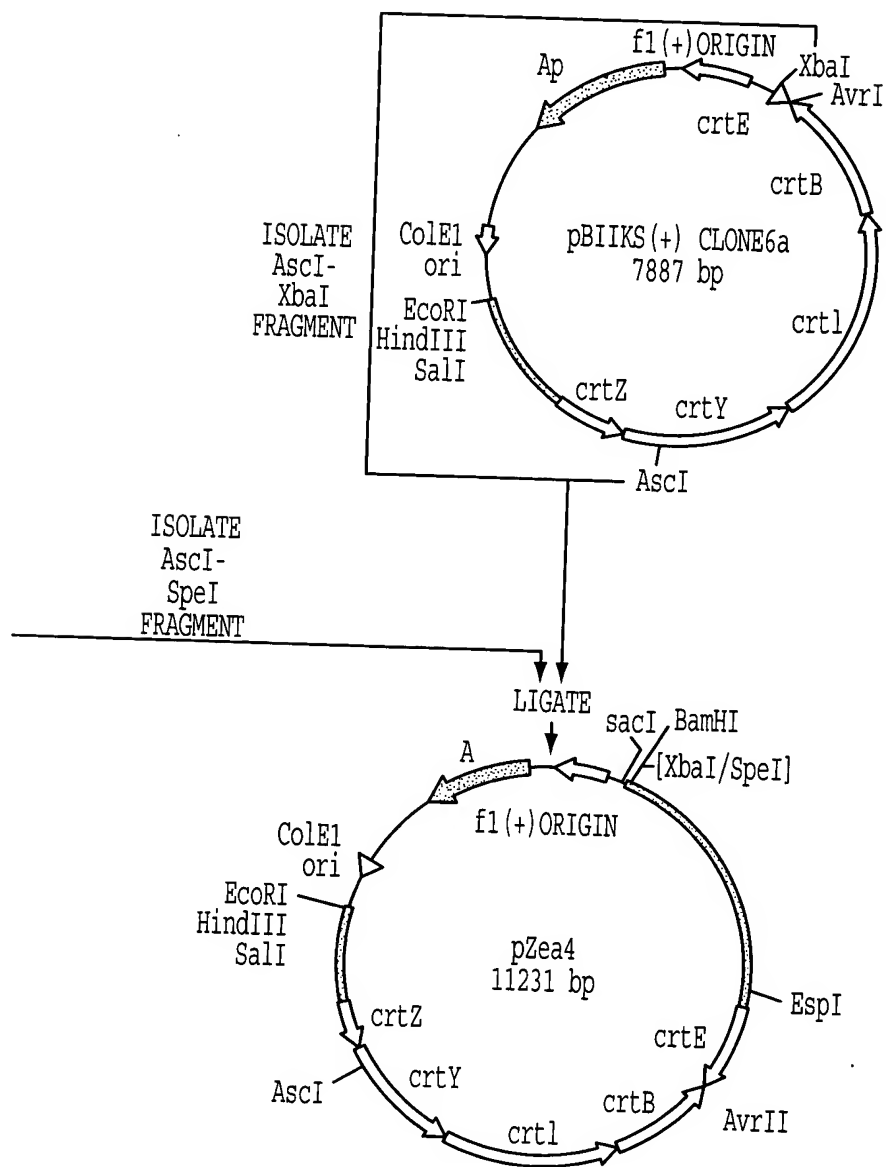
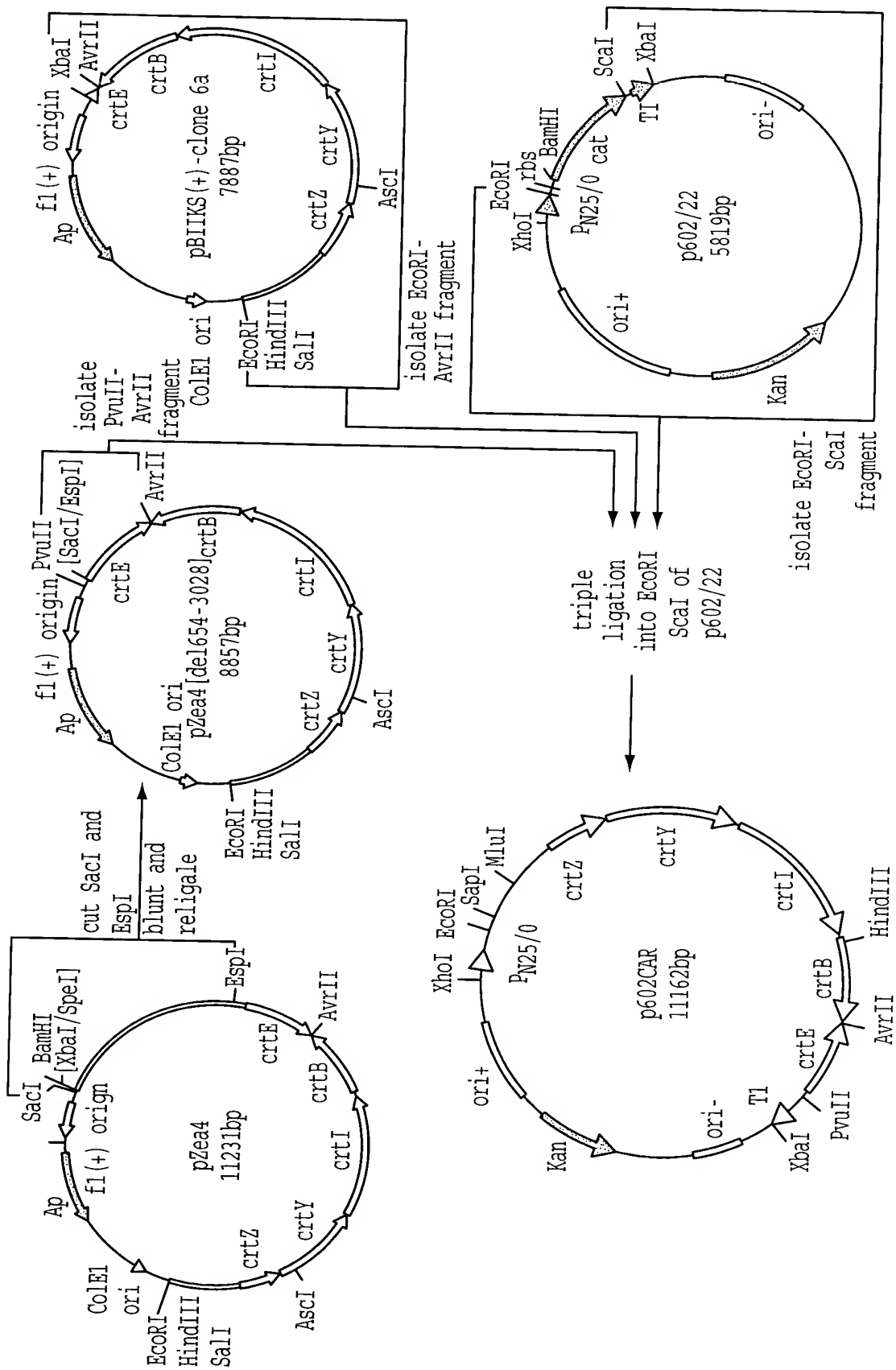


FIG. 16A



**FIG. 16B**



**FIG. 17**



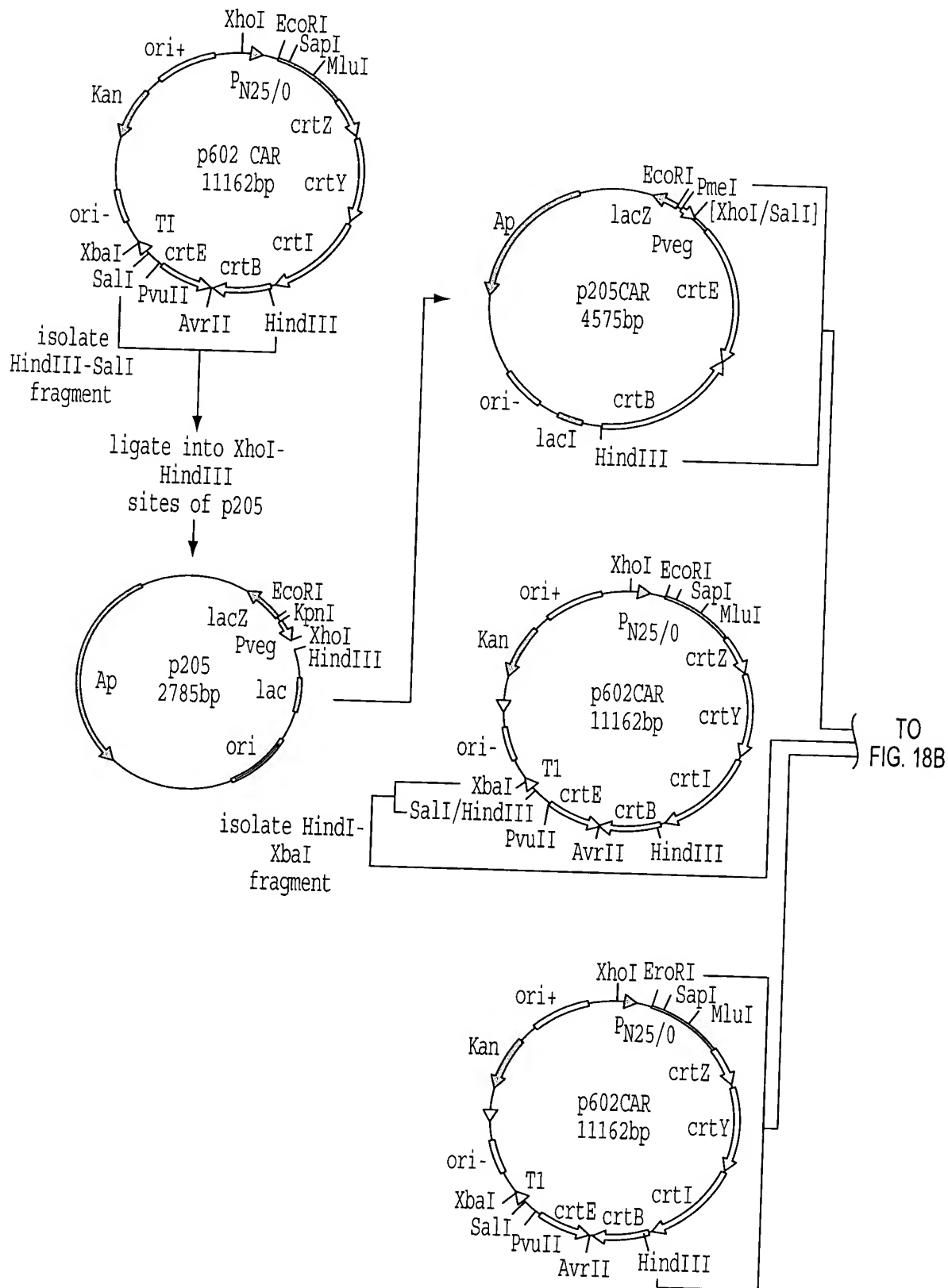


FIG. 18A

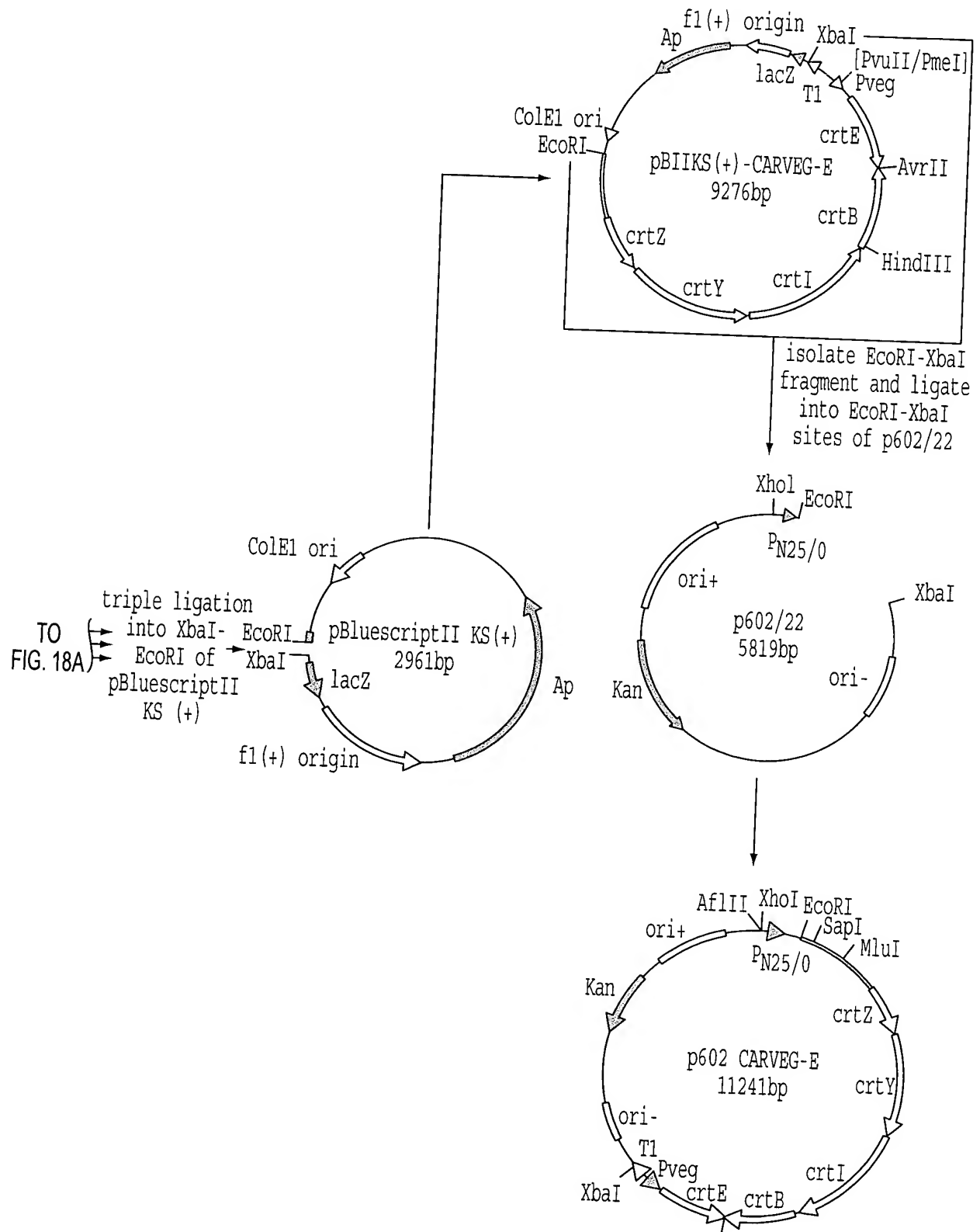


FIG. 18B

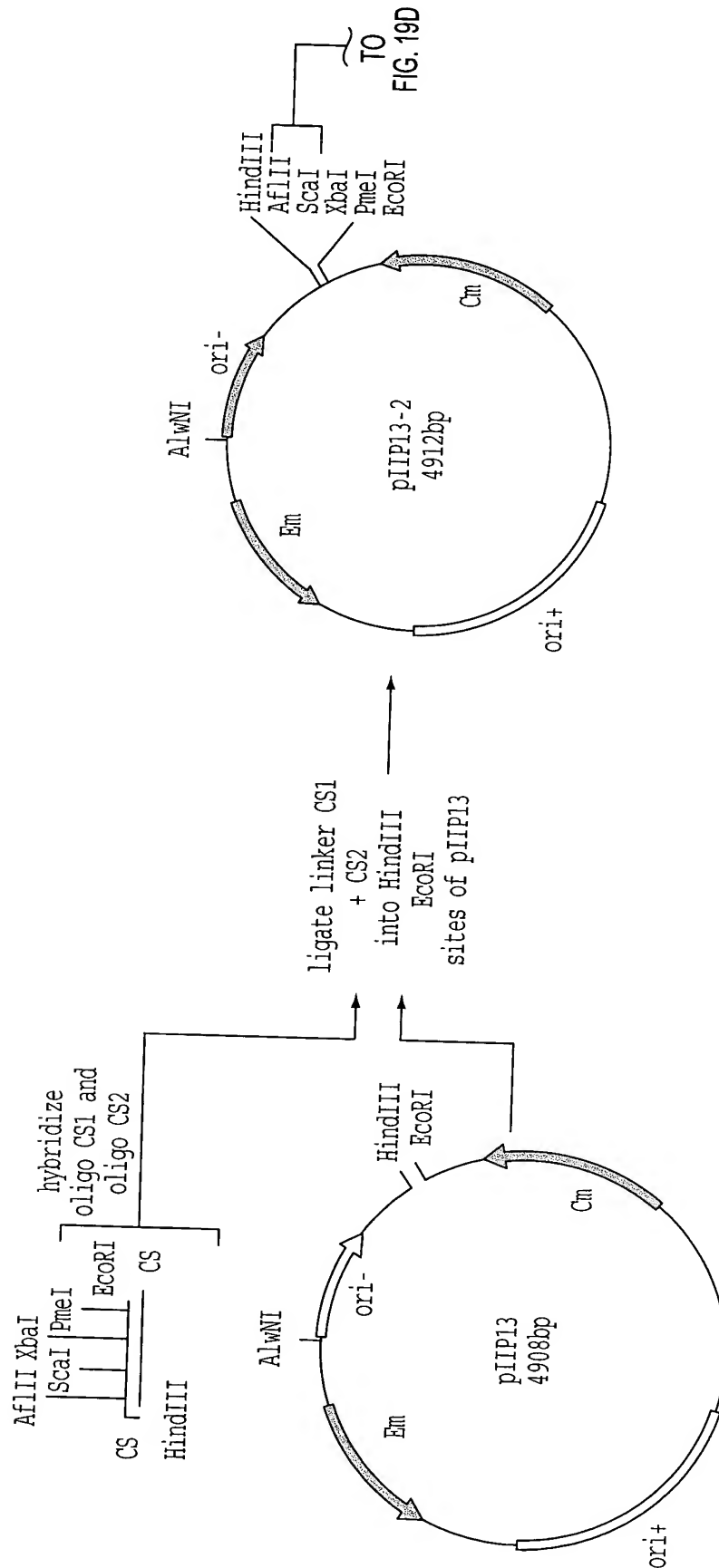
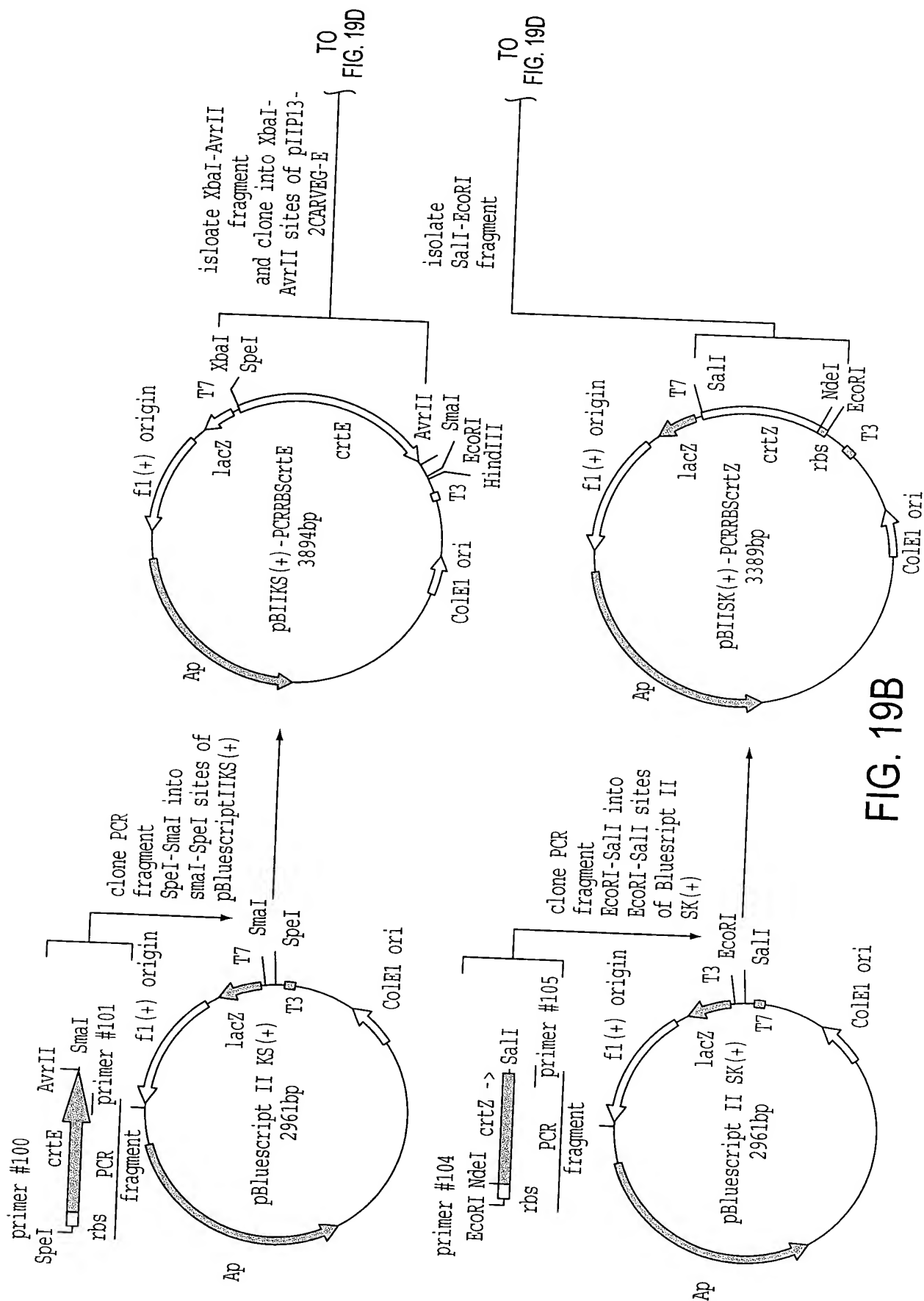


FIG. 19A



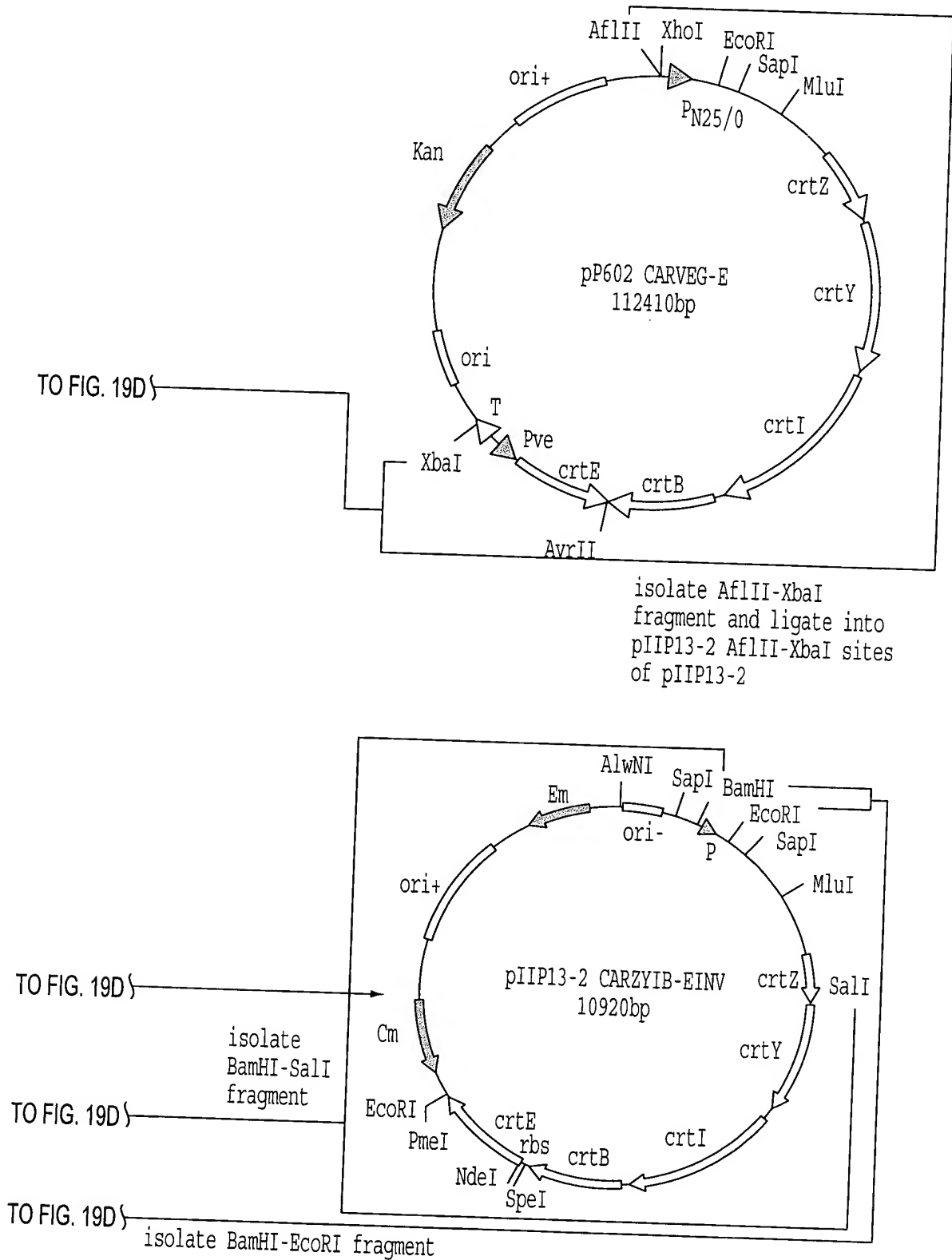
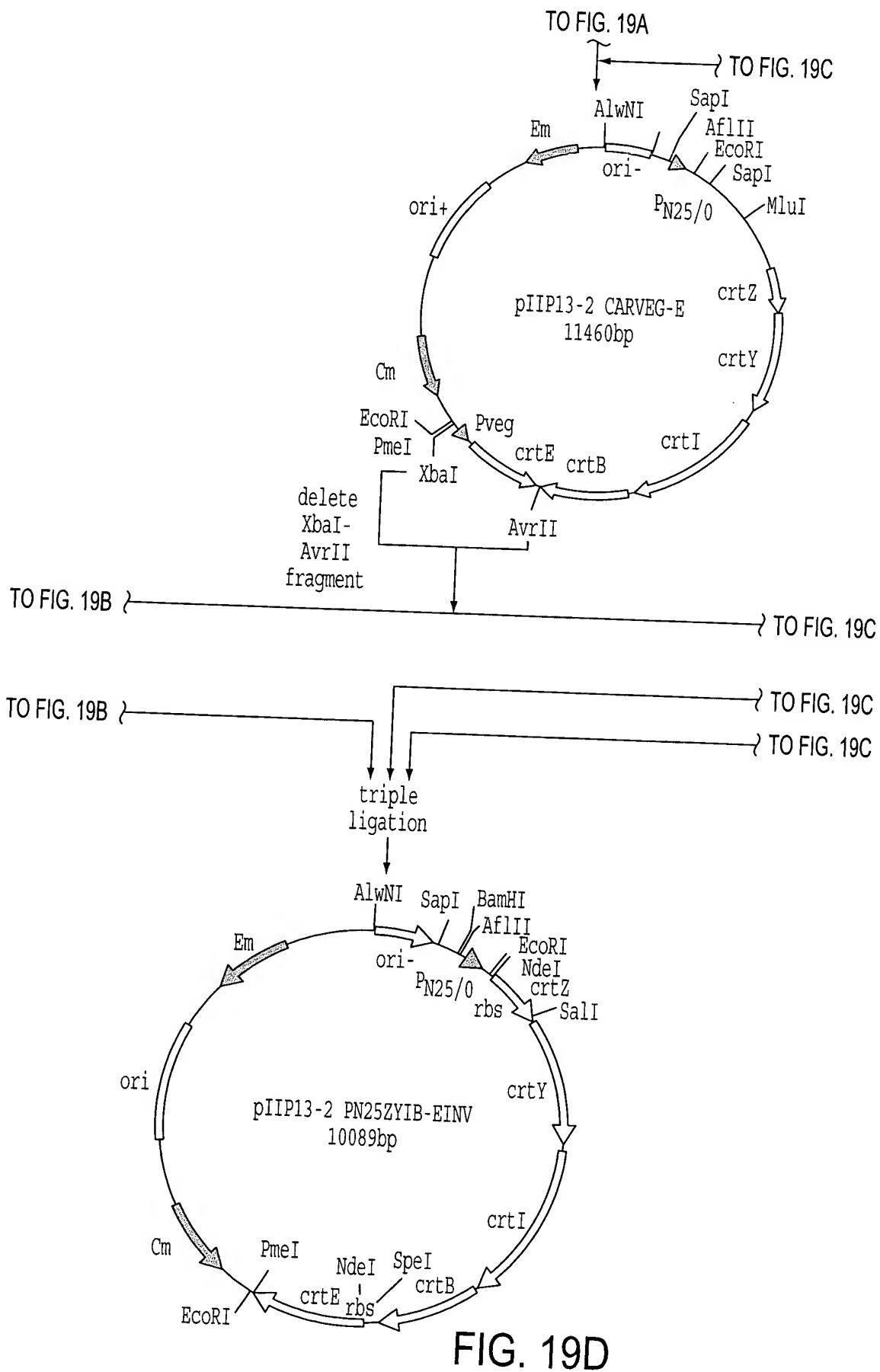


FIG. 19C



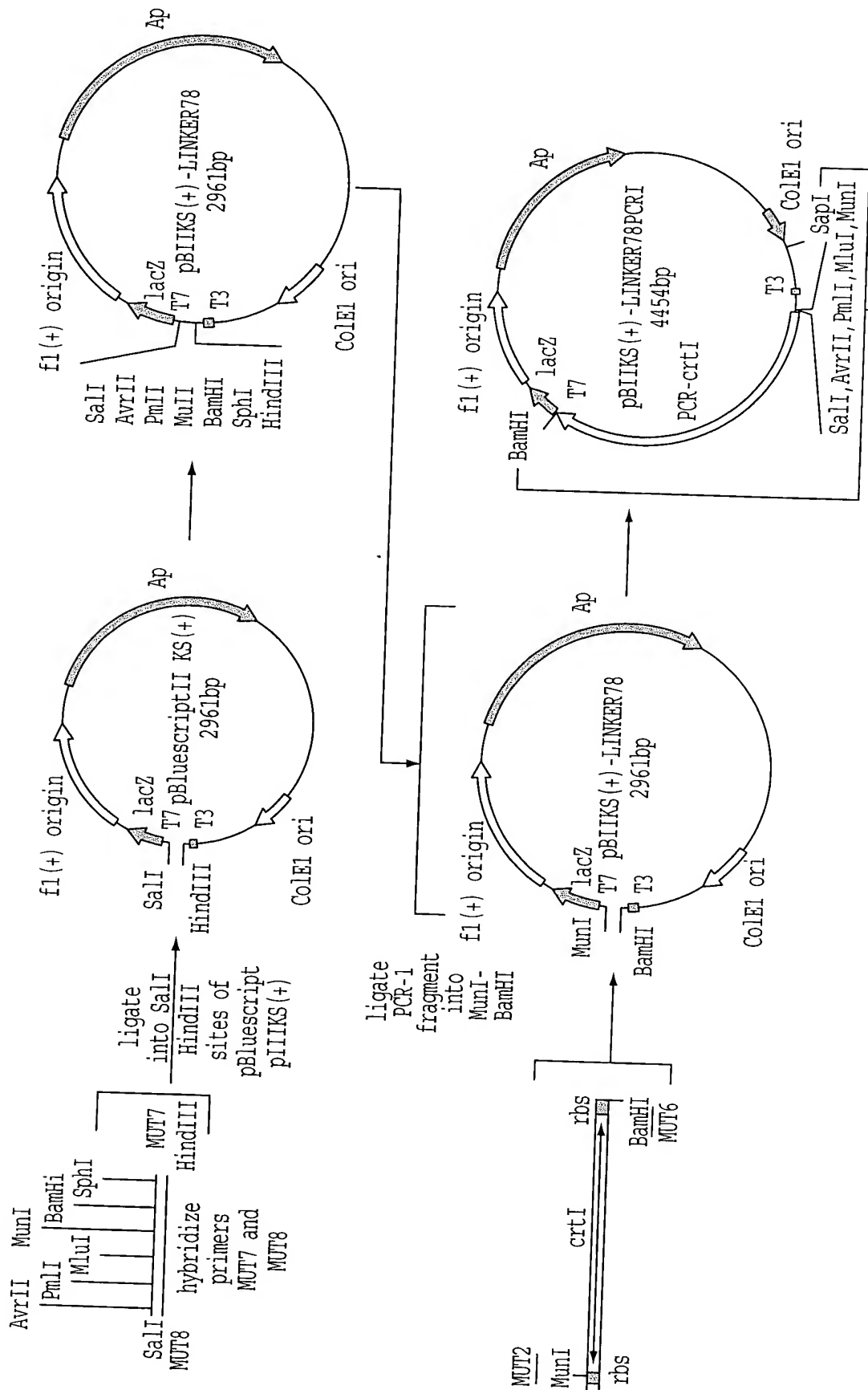


FIG. 20A-1

TO FIG. 20A-2

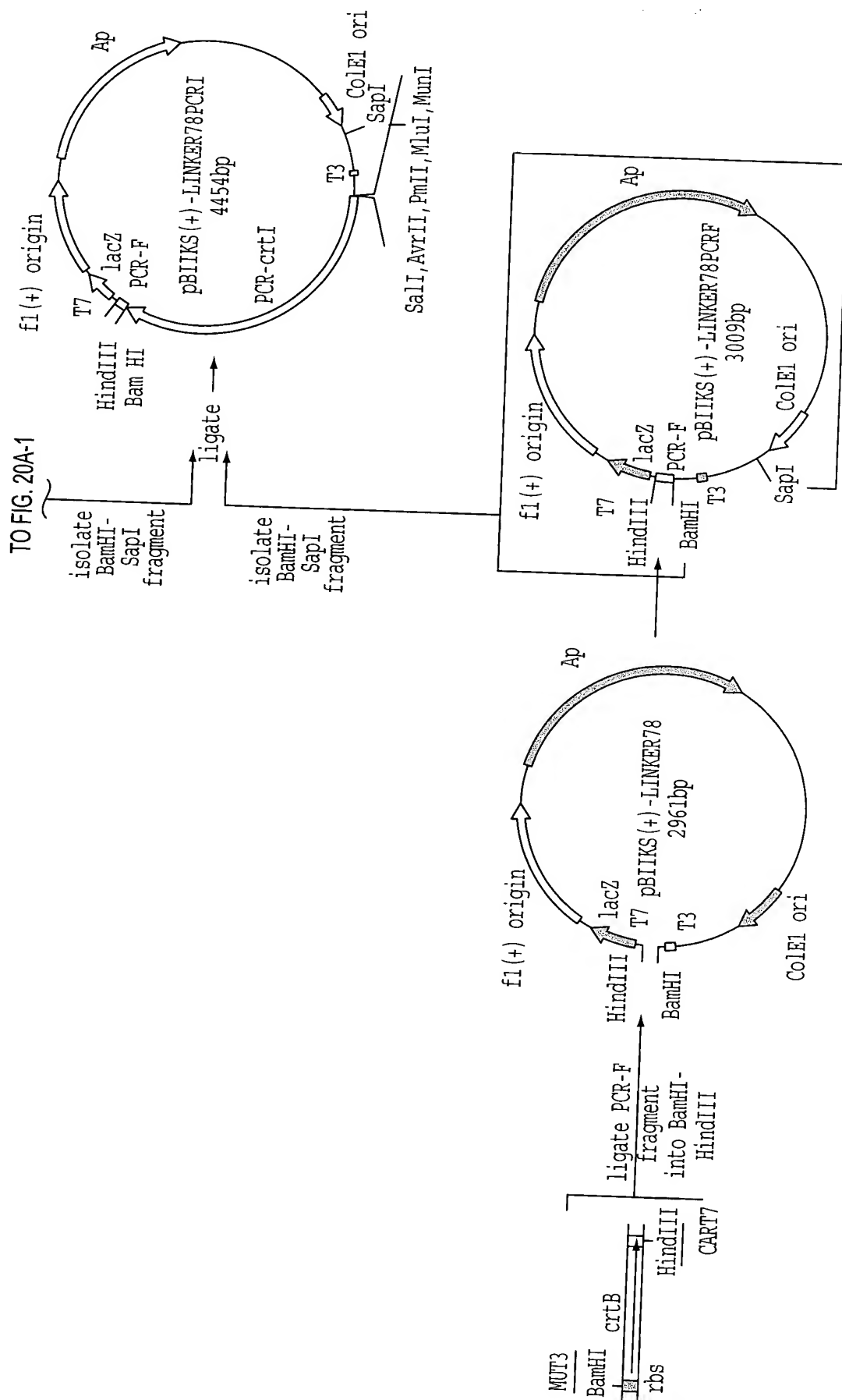


FIG. 20A-2



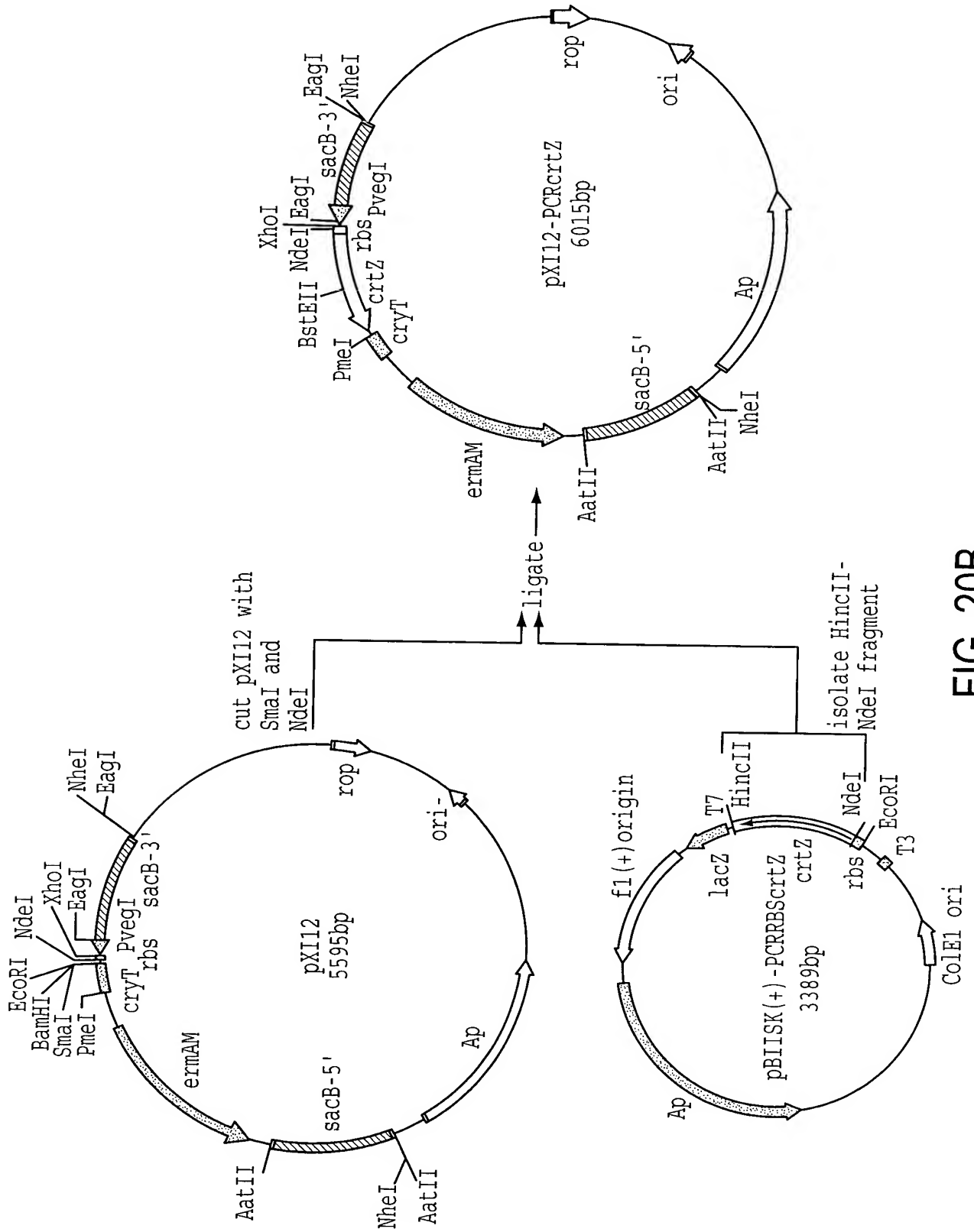


FIG. 20B

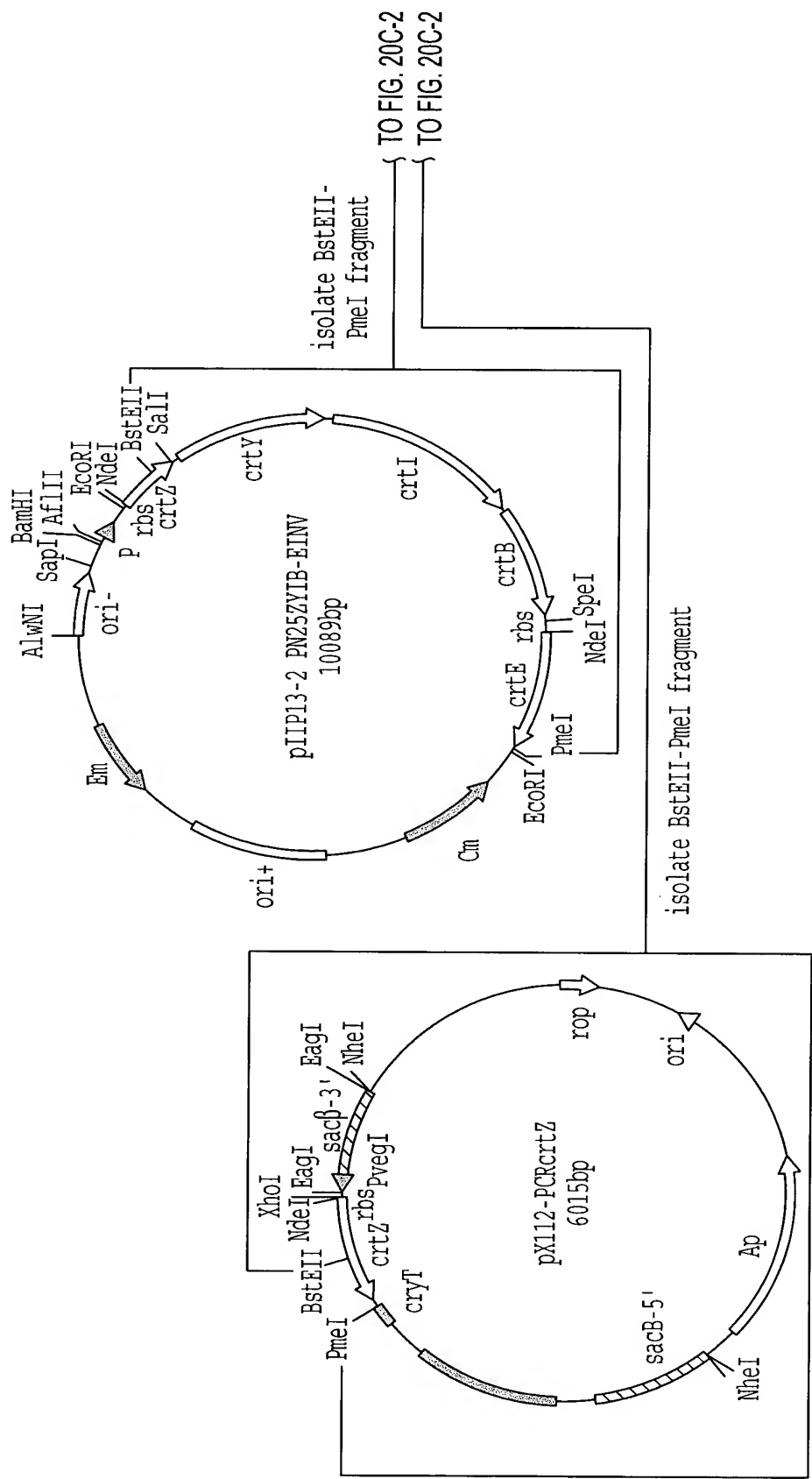


FIG. 20C-1

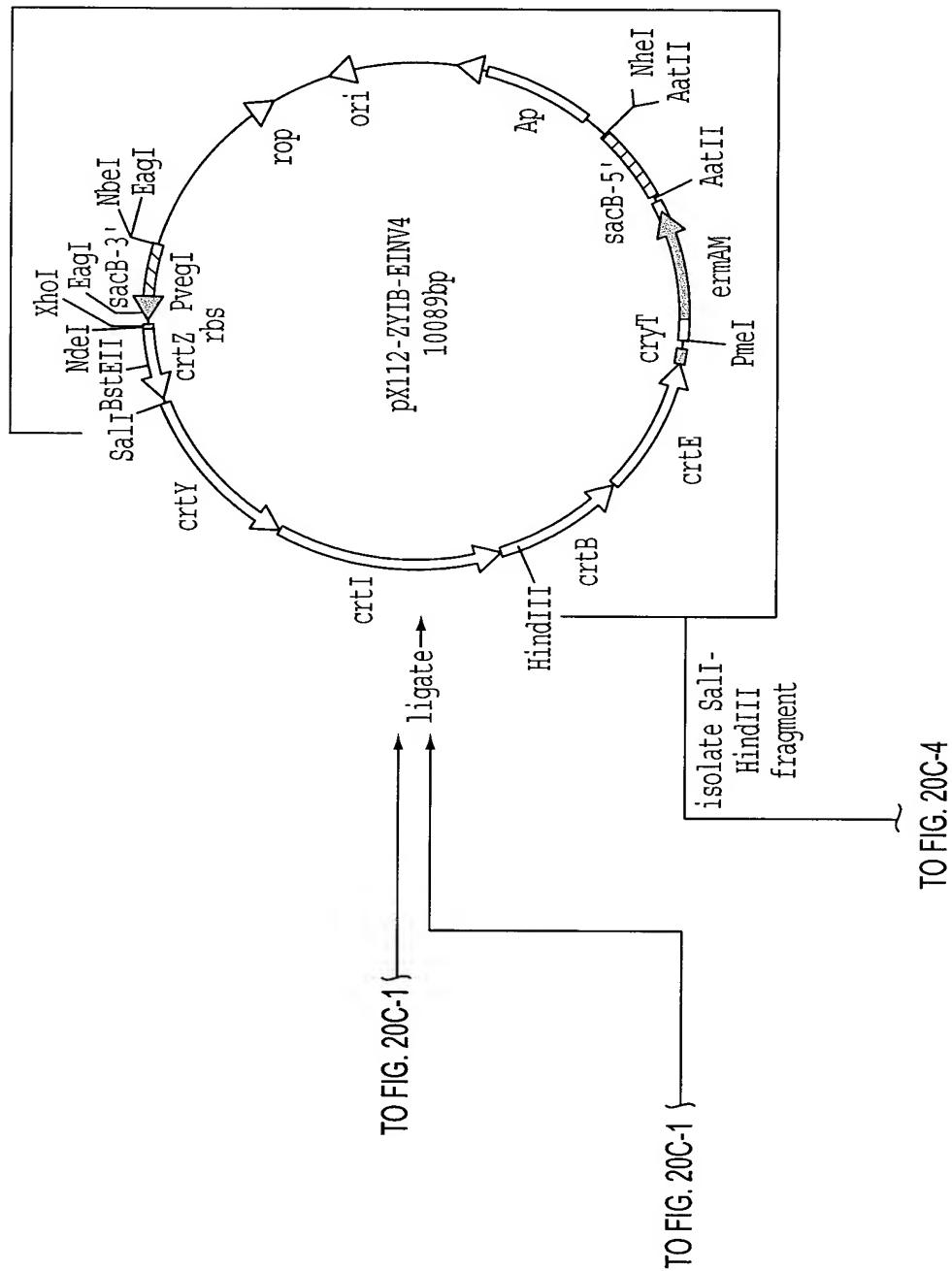


FIG. 20C-2

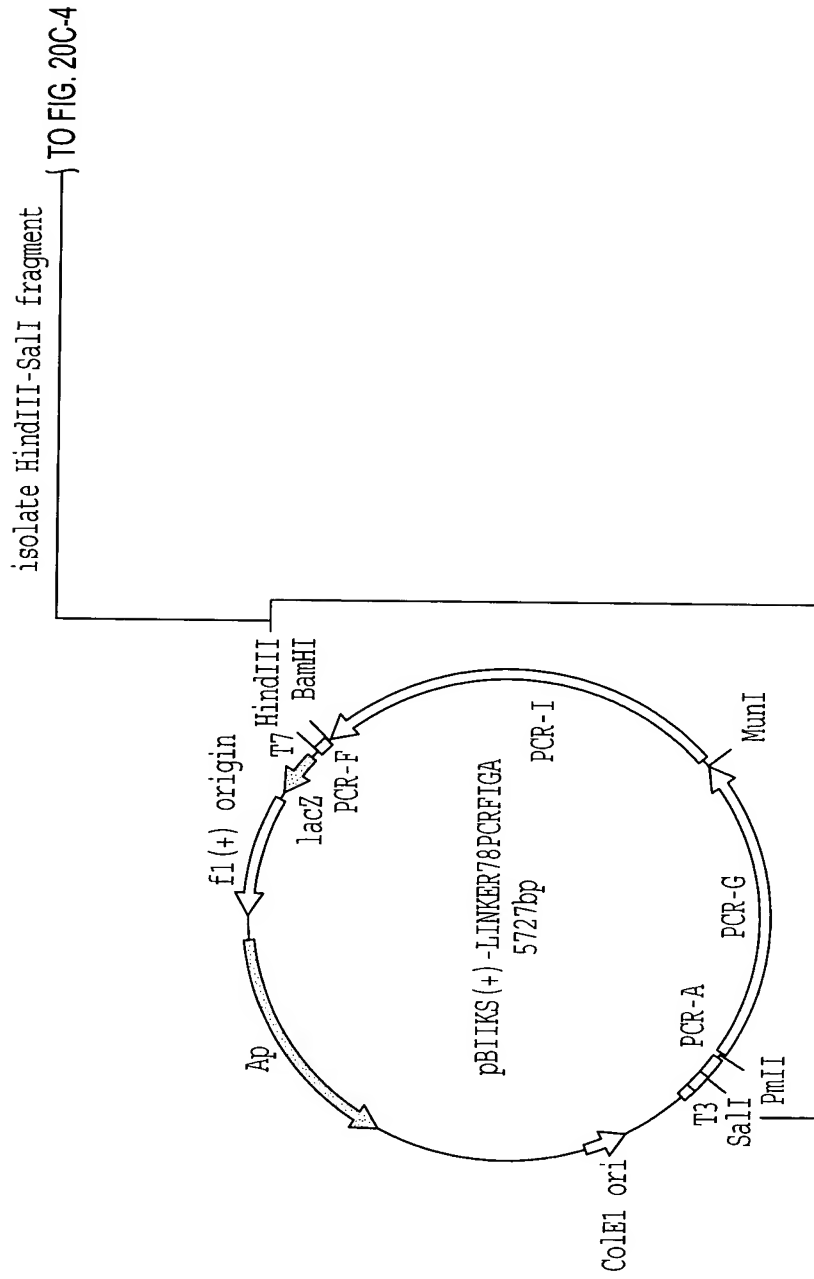
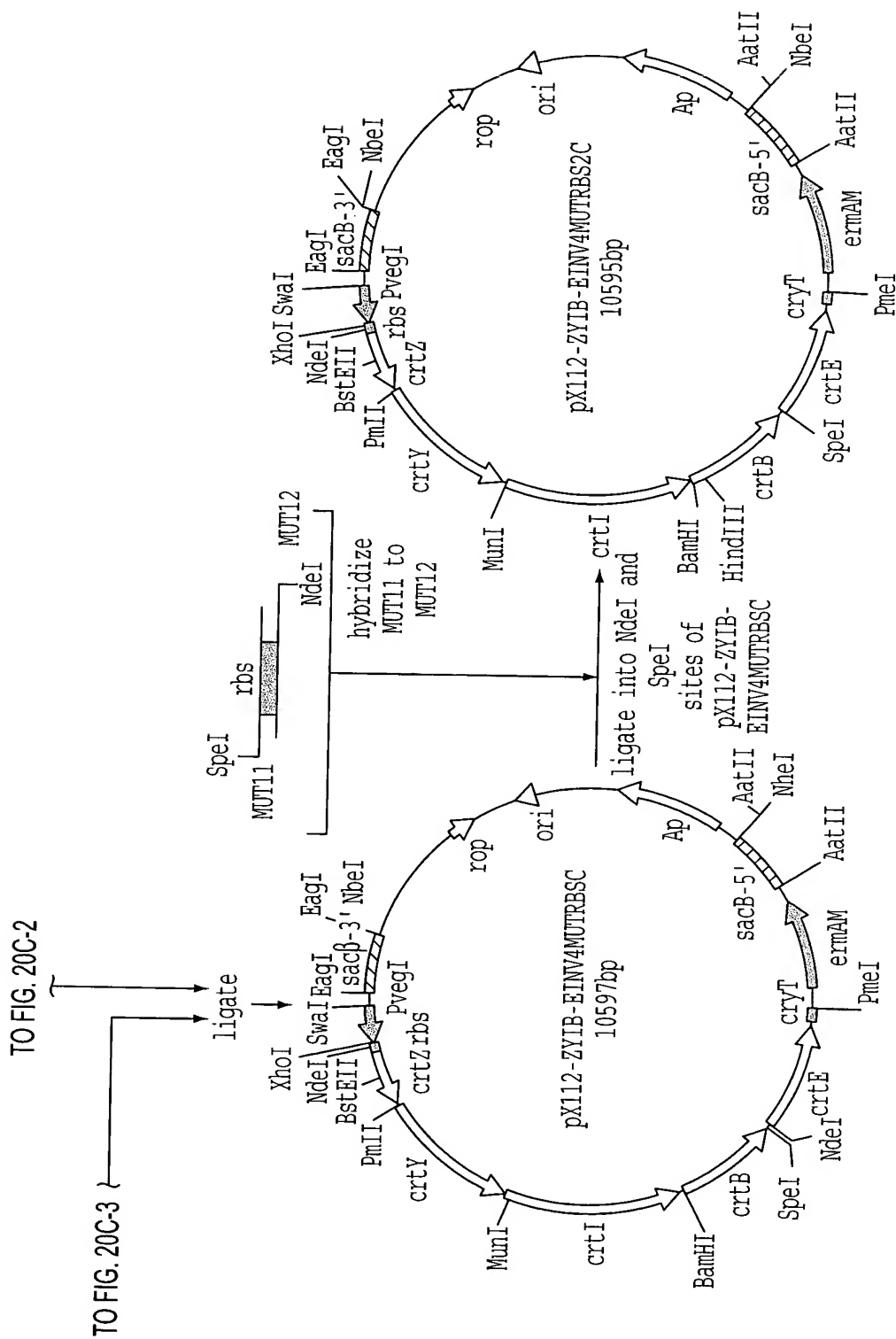


FIG. 20C-3



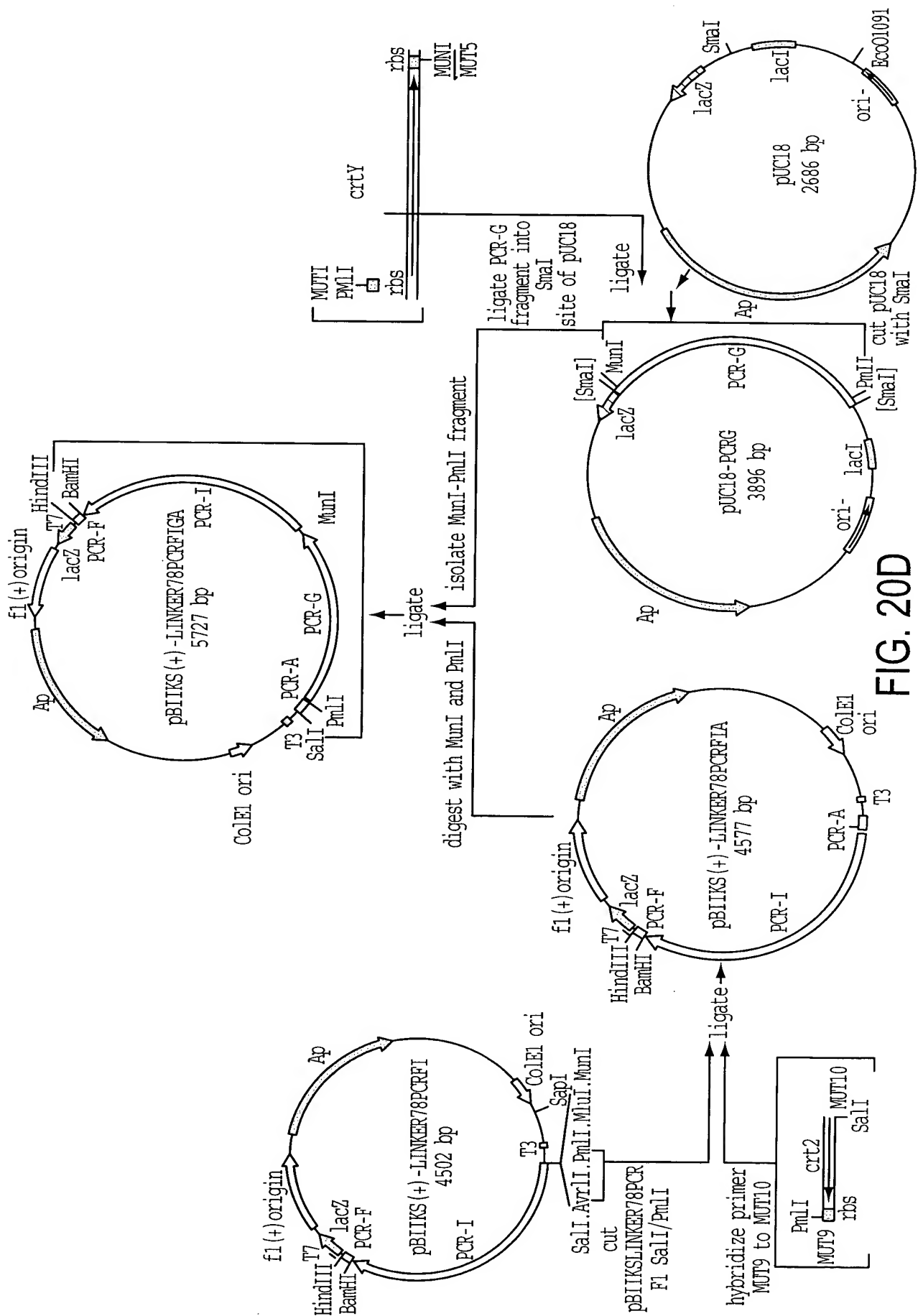


FIG. 20D

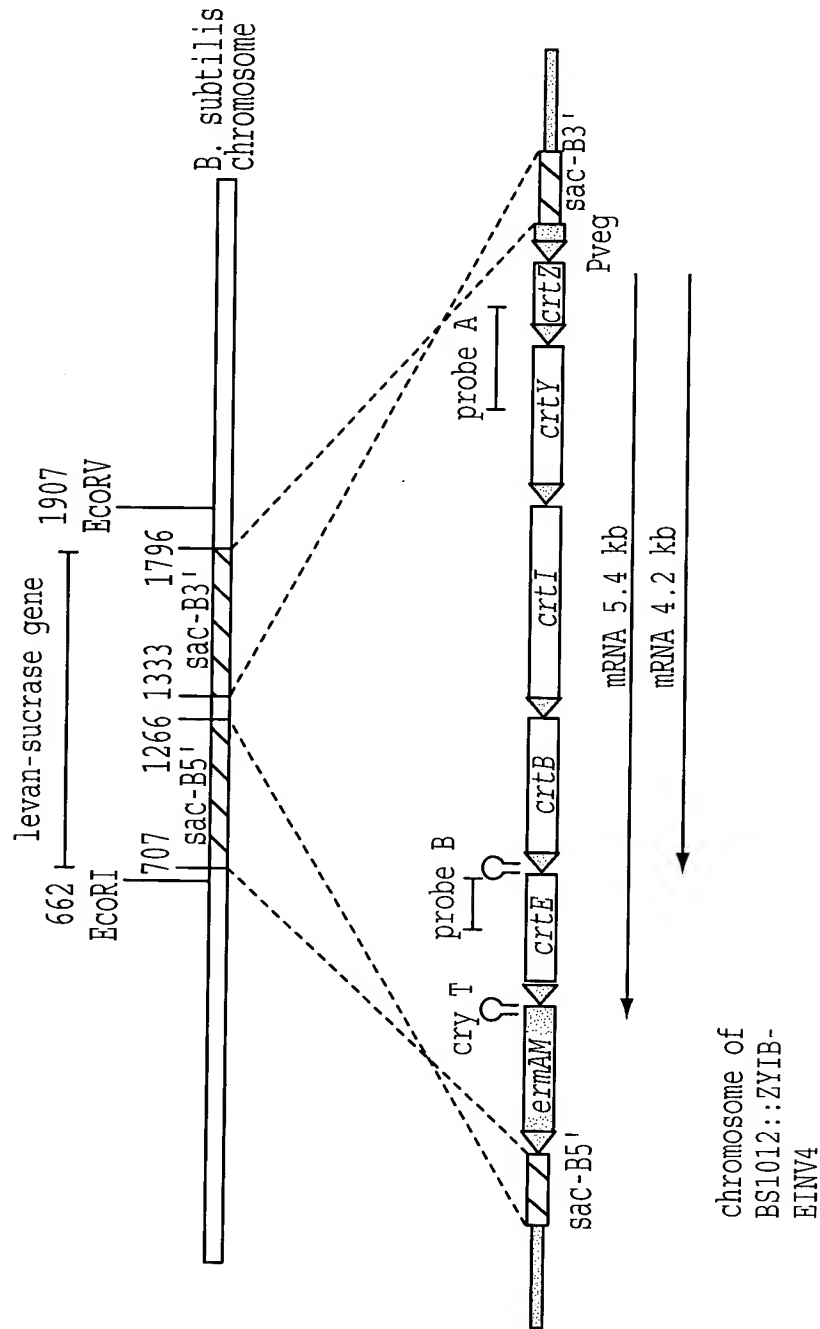


FIG. 21A

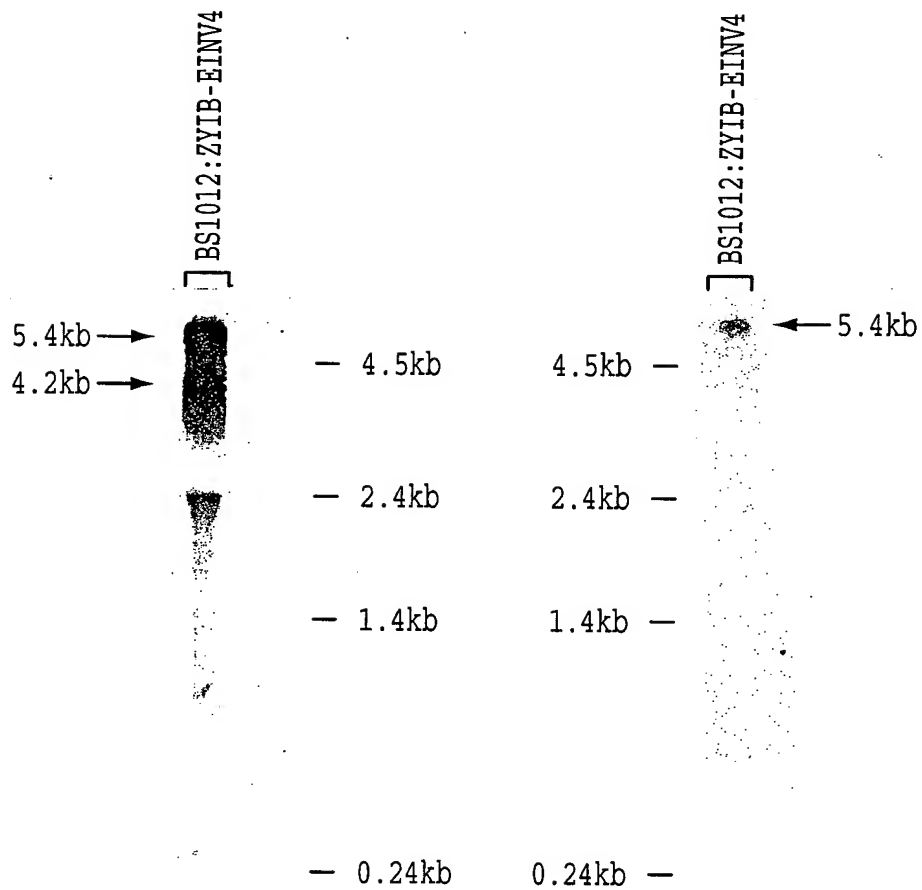


FIG. 21B

FIG. 21C



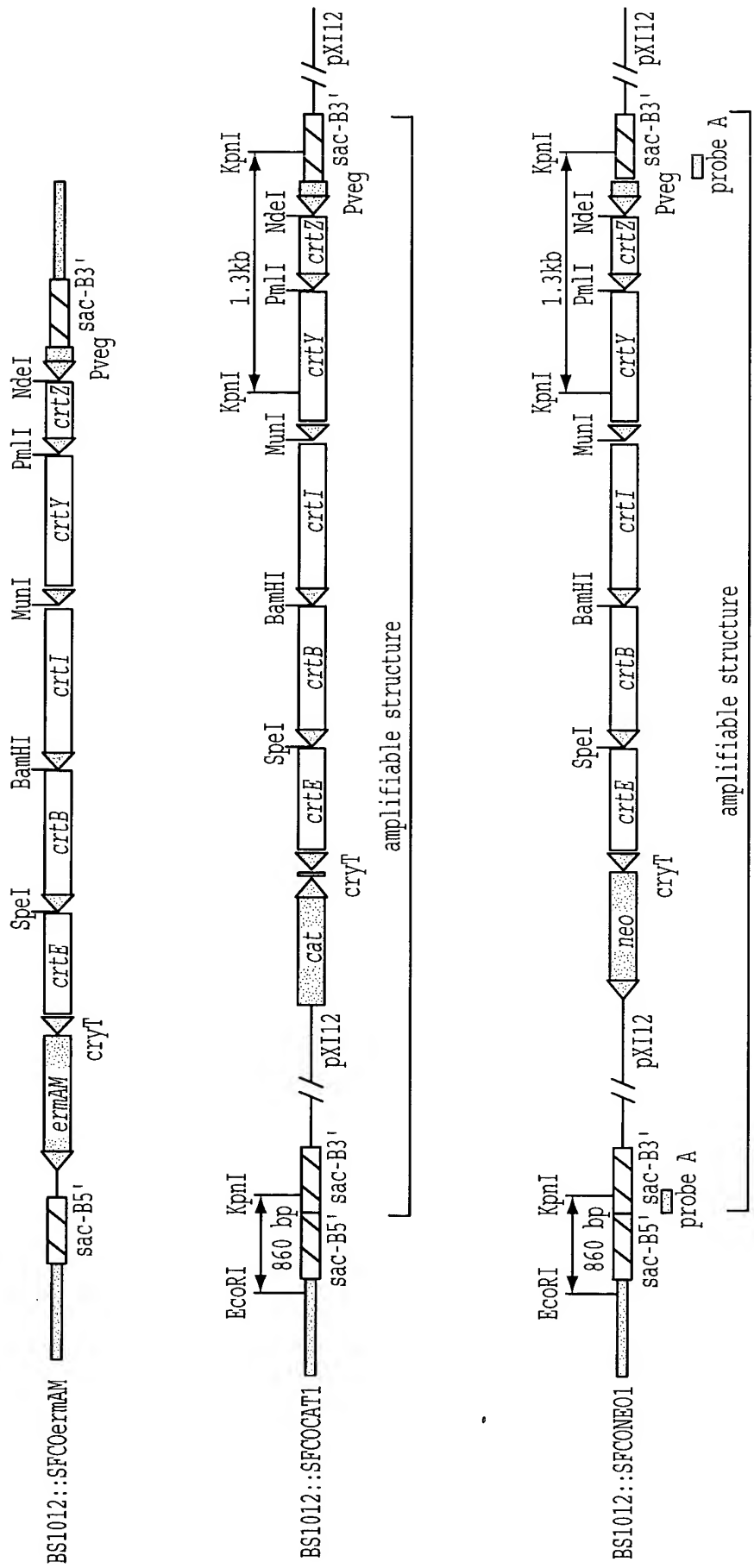


FIG. 22

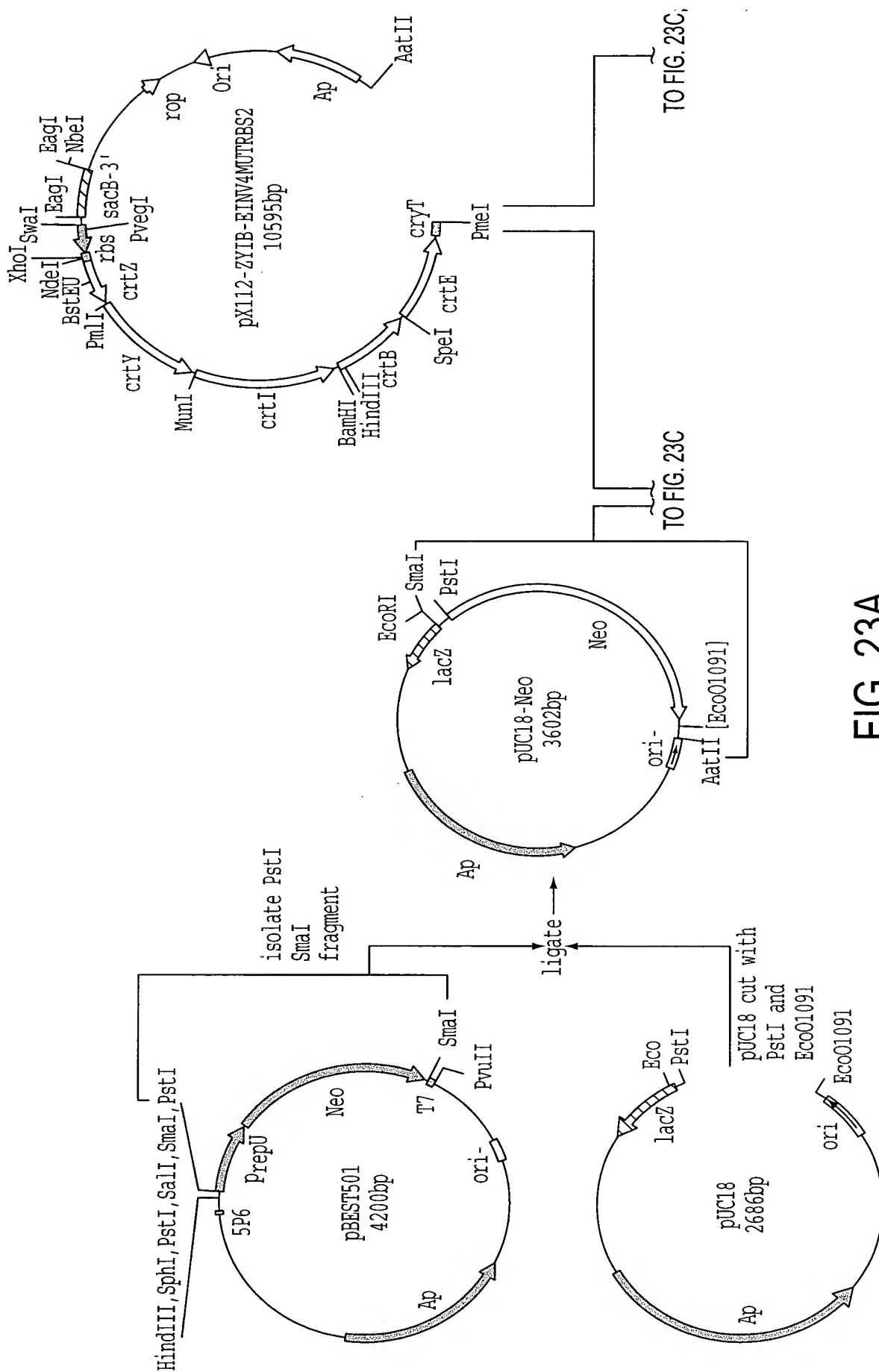
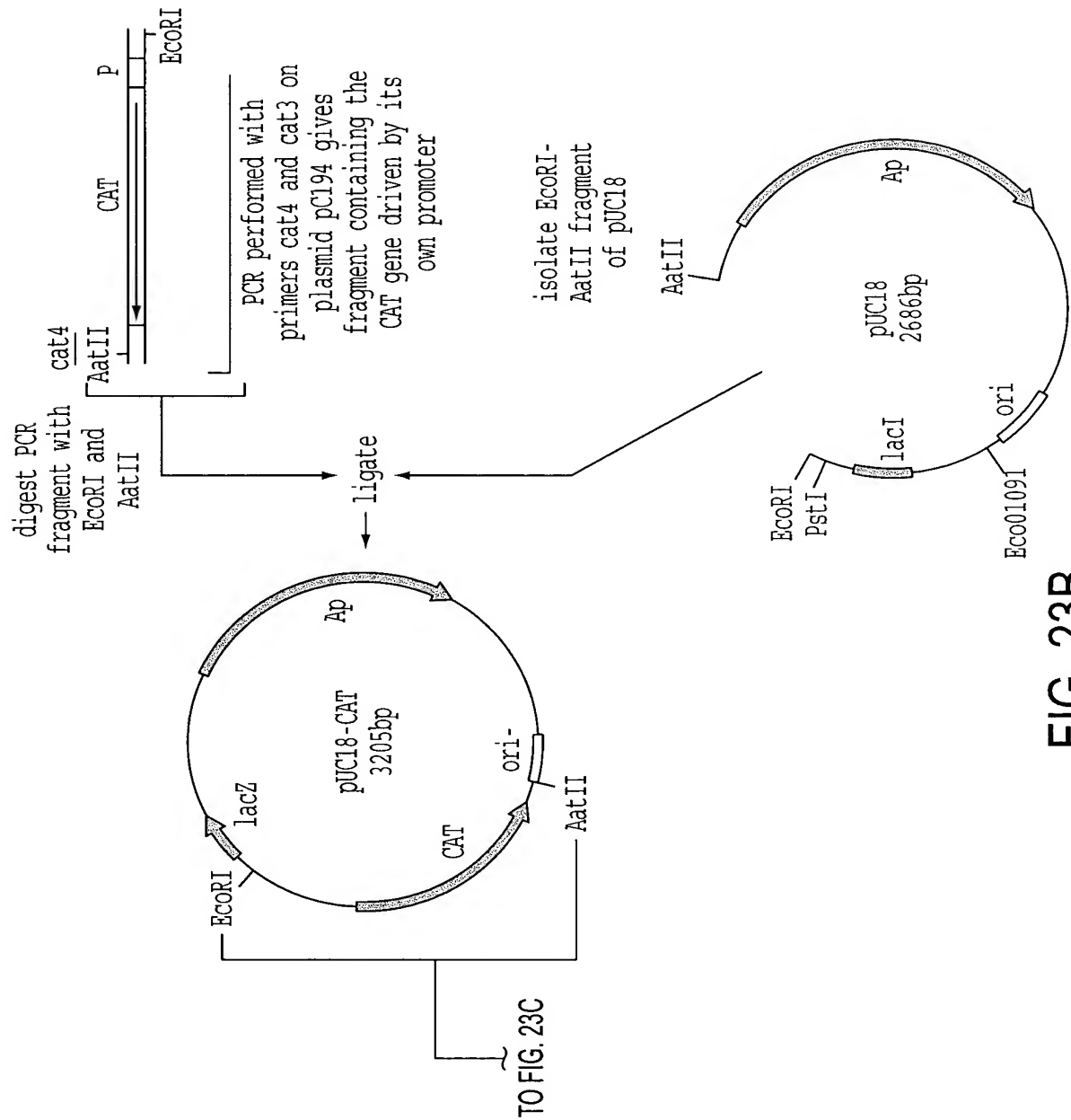


FIG. 23A



**FIG. 23B**

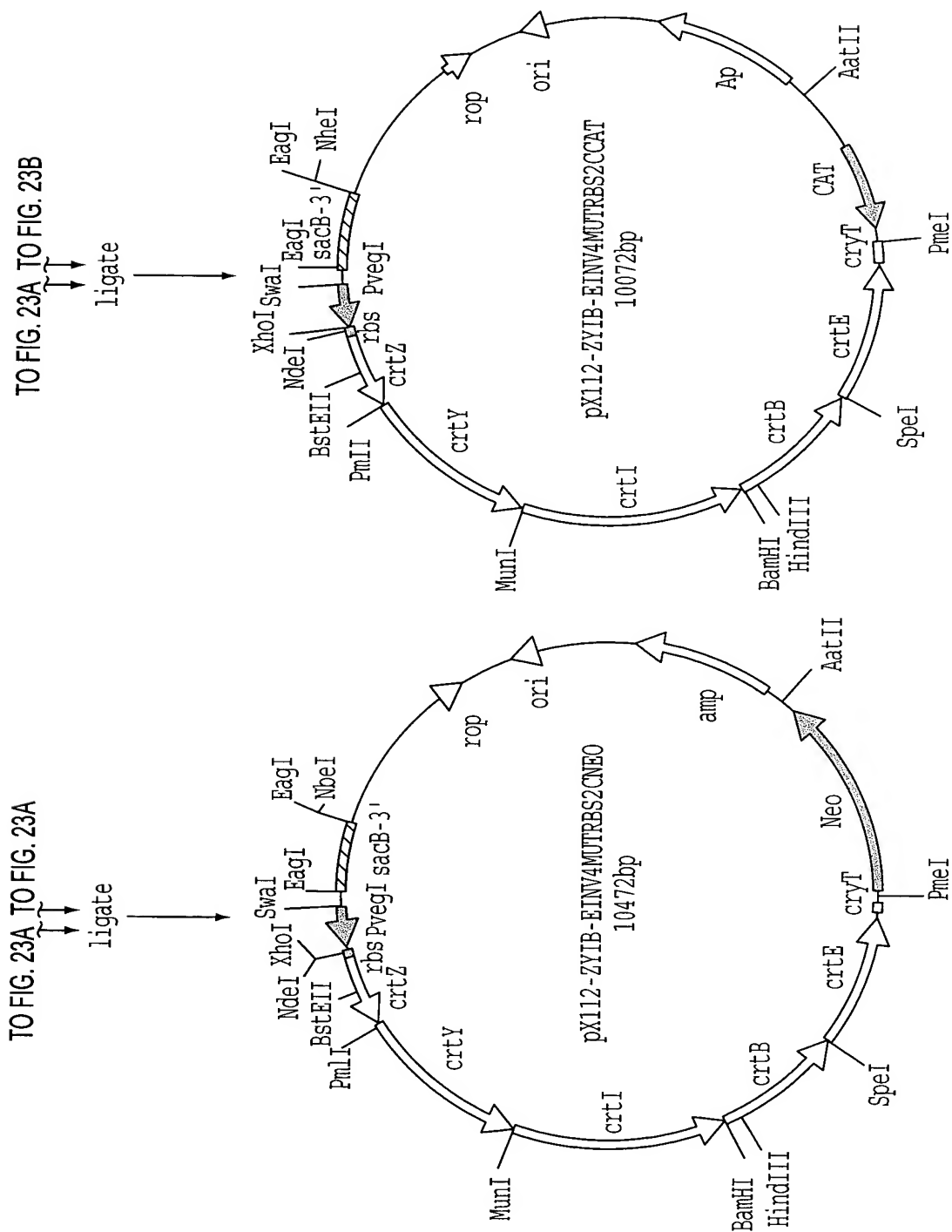


FIG. 23C

```

1  CTAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTGTAAATCAGCTC
   -----+-----+-----+-----+-----+-----+
61  GATTTAACATTTCGAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAG
   -----+-----+-----+-----+-----+-----+
   ATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGA
121 -----+-----+-----+-----+-----+-----+
   TAAAAAATTGGTTATCCGGCTTTAGCCGTTTtagggaatatTTAGTTTTCTTATCTGGCT
   -----+-----+-----+-----+-----+-----+
181 GATAGGGTTGAGTGTTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTC
   -----+-----+-----+-----+-----+-----+
   CTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAG
   -----+-----+-----+-----+-----+-----+
241 CAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACC
   -----+-----+-----+-----+-----+-----+
   GTTGCGAGTTTCCCGCTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGG
   -----+-----+-----+-----+-----+-----+
301 CTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGGAG
   -----+-----+-----+-----+-----+-----+
   GATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCTC
   -----+-----+-----+-----+-----+-----+
361 CCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAA
   -----+-----+-----+-----+-----+-----+
   GGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCAACCGCTCTTCTCCTTCCCTTCTT
   -----+-----+-----+-----+-----+-----+
421 AGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGtagCGGTcACGCTGCGCGTAACCAC
   -----+-----+-----+-----+-----+-----+
   TCGCTTTCCTCGCCCGCATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTTGGTG
   -----+-----+-----+-----+-----+-----+
481 CACACCCGCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCATTcAGGCTGCG
   -----+-----+-----+-----+-----+-----+
   GTGTGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGGGTAAGCGGTAAGTCCGACGC
   -----+-----+-----+-----+-----+-----+
541 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG
   -----+-----+-----+-----+-----+-----+
   GTTGACAACCCTTCCCGCTAGCCACGCCCCGAGAAGCGATAATGCGGTcGACCGCTTTC
   -----+-----+-----+-----+-----+-----+
601 GGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTCACGACGTTG
   -----+-----+-----+-----+-----+-----+
   CCTTACACGACGTTCCGCTAATTCAACCCATTGCGGTCCCAAAGGGTCAGTGCTGCAAC
   -----+-----+-----+-----+-----+-----+
661 TAAAACGACGGCCAGTGAGCGCGCTAATACGACTCACTATAGGGCGAATTGGAGCTCCA
   -----+-----+-----+-----+-----+-----+
   ATTTTGCTGCCGGTCACTCGCGCGATTATGCTGAGTGATATCCCGCTTAACCTCGAGGT
   -----+-----+-----+-----+-----+-----+
721 CCGCGGTGGCGGCCGCTCTAGTGGATCCGCGCCTGGCCGTTTCGCGATCAGCAGCCGCCCT
   -----+-----+-----+-----+-----+-----+
   GGCGCCACCGCCGGCGAGATCACCTAGGCGCGGACCGGCAAGCGCTAGTCGTGCGCGGGA
   -----+-----+-----+-----+-----+-----+
781 TGCGGATCGGTCAGCATCATCCCCATGAACCGCAGCGCACGACGCGCGCGCCCCAGA
   -----+-----+-----+-----+-----+-----+
   ACGCCTAGCCAGTCGTAGTAGGGGTACTTGGCGTCGCGTGCTGCGTCGCGCGGGGTCT
   -----+-----+-----+-----+-----+-----+
841 TCGGGCGCGTCCAGCACGGCATGCGCCATCATCGGAAGGCCCCCGGCGGCATGGGGCGC
   -----+-----+-----+-----+-----+-----+
   AGCCCGCGCAGGTCTGTCCGTACGCGGTAGTAGCGCTTCCGGGGCCGCGTACCCCGCG
   -----+-----+-----+-----+-----+-----+
901 GTGCCCATTCCGAAGAACTCGCAGCCTGTCCGCTGCGCAAGGTGCGGCCAGATCGCGCCG
   -----+-----+-----+-----+-----+-----+
   CACGGGTAAAGGCTTCTTGAGCGTCGGACAGGCGACGCGTTCAGCGCGGTCTAGCGCGGC
   -----+-----+-----+-----+-----+-----+
961 TATTCCGATGCAGTGACGGGCCCCGATGCGCGTGGGCCCCGCCCTGCCCCGCCGCCACCAGC
   -----+-----+-----+-----+-----+-----+
   ATAAGGCTACGTCACTGCCCCGGGTACGCGCACCCGGGCGGGACGGGGCGGCGGTGGTTCG

```

**FIG. 24A**

961 GCATCGCGCACGAACCCCTCCGAGATGATGTGCTGATCCATGGCCCGTCATTGCAAAACC 1020  
 CGTAGCGCGTGCTTGGGAAGGCTCTACTACACGACTAGGTACCGGGCAGTAACGTTTTGG  
 1021 GATCACCGATCCTGTCGCGTGATGGCATTGTTTGCAATGCCCCGAGGGCTAGGATGGCGC 1080  
 CTAGTGGCTAGGACAGCGCACTACCGTAACAAACGTTACGGGGCTCCCGATCCTACCGCG  
 1081 GAAGGATCAAGGGGGGAGAGACATGGAATCGAGGGACGGGTCTTTGTCGTCACGGGCG 1140  
 CTTCTAGTTCCCCCCTCTCTGTACCTTTAGCTCCCTGCCAGAAACAGCAGTGCCCGC  
 1141 CCGCATCGGGTCTGGGGGCGGCCCTCGGCGCGGATGCTGGCCCAAGGCGGCGCGAAGGTCG 1200  
 GCGTAGCCCGAGACCCCGCCGGAGCCGCGCCTACGACCGGGTTCCGCCGCGCTTCCAGC  
 1201 TGCTGGCCGATCTGGCGGAACCGAAGGACGCGCCCGAAGGCGCGGTTACGCGGCCCTGCG 1260  
 ACGACCGGCTAGACCGCCTTGGCTTCTGCGGGGCTTCCGCCCAAGTGCGCCGACGC  
 1261 ACGTGACCGACGCGACCGCTGCGCAGACGGCCATCGCGCTGGCGACCGACCGCTTCGGCA 1320  
 TGCCTGGCTGCGCTGGCGACGCGTCTGCCGGTAGCGCGACCGCTGGCTGGCGAAGCCGT  
 1321 GGCTGGACGGCCTTGTGAACTGCGCGGGCATCGCGCCGGCCGAACGGATGCTGGGCCGCG 1380  
 CCGACCTGCCGGAACACTTGACGCGCCCGTAGCGGGCCGGCTTGCCCTACGACCCGGCGC  
 1381 ACGGGCCGCATGGACTGGACAGCTTTGCCCGTGGGTACGATCAACCTGATCGGCAGCT 1440  
 TGCCCGGCGTACCTGACCTGTGAAACGGGCACGCCAGTGCTAGTTGGAAGTAGCCGTGCA  
 1441 TCAACATGGCCCGCCTTGACAGCCGAGGCGATGGCCCGAACGAGCCCGTCCGGGGCGAGC 1500  
 AGTTGTACCGGGCGGAACGTGCGCTCCGCTACCGGGCCTTGCTCGGGCAGGCCCCGCTCG  
 1501 GTGGCGTGATCGTCAACACGGCCTCGATCGCGGCGCAGGACGGACAGATCGGACAGGTCG 1560  
 CACCGCACTAGCAGTTGTGCCGGAGTAGCGCCGCGTCTGCCTGTCTAGCCTGTCCAGC  
 1561 CCTATGCGGCCAGCAAGGCGGGCGTGGCGGGCATGACGCTGCCGATGGCCCGCGACCTTG 1620  
 GGATACGCCGGTCGTTCCGCCCCGACCGCCCGTACTGCGACGGCTACCGGGCGCTGGAAC  
 1621 CGCGGCACGGCATCCGCGTCATGACCATCGCGCCCGCATCTTCCGACCCCGATGCTGG 1680  
 GCGCCGTGCCGTAGGCGCAGTACTGGTAGCGCGGGCCGTAGAAGGCGTGGGGCTACGACC  
 1681 AGGGGCTGCCGAGGACGTTTCAAGACAGCCTGGGCGCGGCGGTGCCCTTCCCCTCGCGGC 1740  
 TCCCCGACGGCGTCTGCAAGTCTGTGCGACCCGCGCCGACGGGAAGGGAGCGCCG  
 1741 TGGGAGAGCCGTCGGAATACGCGGCGCTGTTGACCACATCATCGGAACCCCATGCTGA 1800  
 ACCCTCTCGGCAGCCTTATGCGCCCGACAACGTGGTGTAGTAGCGCTTGGGGTACGACT  
 1801 ACGGAGAGGTCATCCGCCTCGACGGCGCATTGCGCATGGCCCCCAAGTGAAGGAGCGTTT 1860  
 TGCTCTCCAGTAGGCGGAGCTGCCGCGTAACGCGTACCGGGGTTCACTTCTCGCAA  
 1861 CATGGACCCCATCGTCATCACGGCGCGATGCGCACCCCGATGGGGGCATTCCAGGGCGA 1920  
 GTACCTGGGGTAGCAGTAGTGGCCGCGCTACGCGTGGGGCTACCCCGTAAGGTCCCGCT  
 1921 TCTTGCCGCGATGGATGCCCCGACCCTTGGCGCGGACGCGATCCGCGCCGCGCTGAACGG 1980  
 AGAACGGCGCTACCTACGGGGCTGGGAACCGCGCCTGCGCTAGGCGCGGCGGACTTGCC

**FIG. 24B**

```

1981 CCTGTCGCCCCGACATGGTGGACGAGGTGCTGATGGGCTGCGTCCTCGCCGCGGGCCAGGG 2040
-----+-----+-----+-----+-----+
GGACAGCGGGCTGTACCACCTGCTCCACGACTACCCGACGCAGGAGCGGCGCCCGGTCCC

2041 TCAGGCACCGGCACGT CAGGCGGCGCTTGGCGCCGGACTGCCGCTGTCGACGGGCACGAC 2100
-----+-----+-----+-----+-----+
AGTCCGTGGCCGTGCAGTCCGCCGCGAACCGCGGCCTGACGGCGACAGCTGCCCCGTGCTG

2101 CACCATCAACGAGATGTGCGGATCGGGCATGAAGGCCGCGATGCTGGGCCATGACCTGAT 2160
-----+-----+-----+-----+-----+
GTGGTAGTTGCTCTACACGCCTAGCCCGTACTTCCGGCGCTACGACCCGGTACTGGACTA

2161 CGCCGCGGGATCGGCGGGCATCGTCGTCGCCGCGGGATGGAGAGCATGTGAAACGCCCC 2220
-----+-----+-----+-----+-----+
GCGGCGCCCTAGCCGCCCGTAGCAGCAGCGCCGCCCTACCTCTCGTACAGCTTGCGGGG

2221 CTACCTGCTGCCCAGGCGCGGTGCGGGATGCGCATGGGCCATGACCGTGTGCTGGATCA 2280
-----+-----+-----+-----+-----+
GATGGACGACGGGTTCCGCGCCAGCCCCTACGCGTACCCGGTACTGGCACACGACCTAGT

2281 CATGTTCCCTCGACGGGTTGGAGGACGCCTATGACAAGGGCCGCCTGATGGGCACCTTCGC 2340
-----+-----+-----+-----+-----+
GTACAAGGAGCTGCCAACCTCCTGCGGATACTGTTCCCGGCGGACTACCCGTGGAAGCG

2341 CGAGGATTGCGCCGGCGATCACGGTTTCACCCGCGAGGCGCAGGACGACTATGCGCTGAC 2400
-----+-----+-----+-----+-----+
GCTCCTAACGCGGCCGCTAGTGCCAAAGTGGGCGCTCCGCGTCTGCTGATACGCGACTG

2401 CAGCCTGGCCCGCGCGCAGGACGCCATCGCCAGCGGTGCCTTCGCCGCCGAGATCGCGCC 2460
-----+-----+-----+-----+-----+
GTCGGACCGGGCGCGCGTCTGCGGTAGCGGTGCCACGGAAGCGGCGGCTCTAGCGCGG

2461 CGTGACCGTCACGGCACGCAAGGTGCAGACCACCGTCGATACCGACGAGATGCCCGGCAA 2520
-----+-----+-----+-----+-----+
GCACTGGCAGTGCCGTGCGTTCCACGTCTGGTGGCAGCTATGGCTGCTCTACGGGCCGTT

2521 GGCCCGCCCCGAGAAGATCCCCCATCTGAAGCCCGCCTTCCGTGACGGTGGCACGGTCAC 2580
-----+-----+-----+-----+-----+
CCGGGCGGGGCTCTTCTAGGGGGTAGACTTCGGGCGGAAGGCACTGCCACCGTGCCAGTG

2581 GCGGCGAACAGCTCGTCGATCTCGGACGGGGCGGCGGCGCTGGTGATGATGCGCCAGTC 2640
-----+-----+-----+-----+-----+
CCGCCGCTTGTCGAGCAGCTAGAGCCTGCCCCGCCGCGGACCACTACTACGCGGTGAG

2641 GCAGGCCGAGAAGCTGGGCCTGACGCCGATCGCGCGGATCATCGGTGATGCGACCCATGC 2700
-----+-----+-----+-----+-----+
CGTCCGGCTCTTCGACCCGGAAGTGCAGGCTAGCGCGCCTAGTAGCCAGTACGCTGGGTACG

2701 CGACCGTCCCGGCCCTGTTCCCGACGGCCCCCATCGGCGCGATGCGCAAGCTGCTGGACCG 2760
-----+-----+-----+-----+-----+
GCTGGCAGGGCCGACAAGGGCTGCCGGGGGTAGCCGCGCTACGCGTTGACGACCTGGC

2761 CACGGACACCCGCCTTGGCGATTACGACCTGTTGAGGTGAACGAGGCATTGCGCGTCGT 2820
-----+-----+-----+-----+-----+
GTGCCTGTGGGCGGAACCGCTAATGCTGGACAAGCTCCACTTGCTCCGTAAGCGGCAGCA

2821 CGCCATGATCGCGATGAAGGAGCTTGGCCTGCCACACGATGCCACGAACATCAACGGCGG 2880
-----+-----+-----+-----+-----+
GCGGTACTAGCGCTACTTCTCGAACCAGGACGGTGTGCTACGGTGCTTGTAGTTGCCGCC

2881 GGCCTGCGCGCTTGGGCATCCCATCGGCGCGTCCGGGGCGCGGATCATGGTCACGCTGCT 2940
-----+-----+-----+-----+-----+
CCGGACGCGCGAACCCGTAGGGTAGCCGCGCAGCCCCCGCGCCTAGTACCAGTGCAGACGA

2941 GAACGCGATGGCGGCGCGGGGCGCGACGCGCGGGGCGCGCATCCGTCTGCATCGGCGGGGG 3000
-----+-----+-----+-----+-----+
CTTGCGCTACCGCCGCGCCCCGCGCTGCGCGCCCCGGCGTAGGCAGACGTAGCCGCCCCC

```

FIG. 24C

3001 CGAGGCGACGGCCATCGCGCTGGAACGGCTGAGCTAATTCATTTGCGCGAATCCGCGTTT 3060  
GCTCCGCTGCCGGTAGCGCGACCTTGCCGACTCGATTAAAGTAAACGCGCTTAGGCGCAAA  
3061 TTCGTGCACGATGGGGGAACCGGAAACGGCCACGCCTGTTGTGGTTGCGTCGACCTGTCT 3120  
AAGCAGTGCTACCCCTTGGCCTTTGCCGGTGCGGACAACACCAACGCAGCTGGACAGA  
3121 TCGGGCCATGCCCCGTGACGCGATGTGGCAGGCGCATGGGGCGTTGCCGATCCGGTTCGCAT 3180  
AGCCCGGTACGGGCACTGCGCTACACCGTCCGCGTACCCCGCAACGGCTAGGCCAGCGTA  
3181 GACTGACGCAACGAAGGCACCGATGACGCCAAGCAGCAATTCCCCCTACGCGATCTGGT 3240  
CTGACTGCGTTGCTTCCGTGGCTACTGCGGGTTCGTCTTAAGGGGGATGCGCTAGACCA  
3241 CGAGATCAGGCTGGCGCAGATCTCGGGCCAGTTCGGCGTGGTCTCGCCCCGCTCGGCGC 3300  
GCTCTAGTCCGACCGCTCTAGAGCCCGGTCAAGCCGCACAGAGCCGGGGCGAGCCGCG  
3301 GGCCATGAGCGATGCCGCCCTGTCCCCGGCAAACGCTTTCGCGCCGTGCTGATGCTGAT 3360  
CCGGTACTCGCTACGGCGGGACAGGGGGCGTTTGCAGAAAGCGCGGCACGACTACGACTA  
3361 GGTGCGCCGAAAGCTCGGGCGGGTCTGCGATGCGATGGTCGATGCCGCCTGCGCGGTGCA 3420  
CCAGCGGCTTTCGAGCCCGCCCCAGACGCTACGCTACCAGCTACGGCGGACGCGCCAGCT  
3421 GATGGTCCATGCCGCATCGCTGATCTTCGACGACATGCCCTGCATGGACGATGCCAGGAC 3480  
CTACCAGGTACGGCGTAGCGACTAGAAGCTGCTGTACGGGACGTACCTGCTACGGTCCTG  
3481 CCGTTCGCGGTACGCCGCCACCCATGTGCGCCATGGCGAGGGGCGCGCGGTGCTTGGCGG 3540  
GGCAGCGCCAGTCGGGCGGTGGGTACAGCGGTACCGCTCCCCGCGCGCCACGAACGCCC  
3541 CATCGCCCTGATCACCGAGGCCATGCGGATTTTGGGCGAGGCGCGCGGCGGACGCGCGGA 3600  
GTAGCGGGACTAGTGGCTCCGGTACGCCTAAAACCCGCTCCGCGCGCCGCGCTGCGGCCT  
3601 TCAGCGCGCAAGGCTGGTCGCATCCATGTGCGCGCGATGGGACCGGTGGGGCTGTGCGC 3660  
ACTGCGCGGTTCCGACCAGCGTAGGTACAGCGCGGCTACCCTGGCCACCCGACACGCG  
3661 AGGGCAGGATCTGGACCTGCACGCCCCCAAGGACGCCGCCGGGATCGAACGTGAACAGGA 3720  
TCCCGTCTAGACCTGGACGTGCGGGGTTCTGCGGCGGCCCTAGCTTGCACTTGTCTT  
3721 CCTCAAGACCGGCGTGCTGTTGTCGCGGGCCTCGAGATGCTGTCCATTATTAAGGGTCT 3780  
GGAGTTCTGGCCGACGACAAGCAGCGCCCGAGCTCTACGACAGGTAATAATTCCCAGA  
3781 GGACAAGGCCGAGACCGAGCAGCTCATGGCTTCGGGCGTCAGCTTGGTCGGGTCTTCCA 3840  
CCTGTTCCGGCTCTGGCTCGTCGAGTACCGGAAGCCCGCAGTCGAACCAGCCCAGAAGGT  
3841 GTCCTATGACGACCTGCTGGACGTGATCGGCGACAAGGCCAGCACCGGCAAGGATACGGC 3900  
CAGGATACTGCTGGACGACCTGCACTAGCCGCTGTTCCGGTCTGGCCGTTCTATGCCG  
3901 GCGCGACACCGCCGCCCCCGGCCAAAGGGCGGCTGATGGCGGTTCGACAGATGGGCGA 3960  
CGCGCTGTGGCGGCGGGGGCCGGTTTCCCGCCGACTACCGCCAGCCTGTCTACCCGCT  
3961 CGTGGCGCAGCATTACCGCGCCAGCCGCGCGCAACTGGACGAGCTGATGCGCACCCGGCT 4020  
GCACCGCGTCGTAATGGCGCGGTGCGCGCGGTTGACCTGCTCGACTACGCGTGGGCCGA

**FIG. 24D**



```

4021 GTTCCGCGGGGGCAGATCGCGGACCTGCTGGCCCGCTGCTGCCGCATGACATCCGCGG 4080
      +-----+-----+-----+-----+-----+
      CAAGGCGCCCCCGTCTAGCGCCTGGACGACCGGGCGCACGACGGCGTACTGTAGGCGGC
4081 CAGCGCCTAGGCGCGCGGTCCAGGCTCCACAGGCCGTGCGGGCTGATTTGCGCGCCGCGCAG 4140
      +-----+-----+-----+-----+-----+
      GTCGCGGATCCGCGCGCCAGCCAGGTGTCCGGCAGCGCCGACTAAAGCGGGCGCGCTC
4141 GCGCGATGCGGCCGCTCCAAGCCTCCGCGCGCCAGAAGCCCGATCTTGCGAGCCTTCGA 4200
      +-----+-----+-----+-----+-----+
      CGCGCTACGCGGCGCAGGTTCCGAGGCGCGCGGTCTTCGGGCTAGAACCCTCGGAAGCT
4201 CGTGCTGATCCGCTGGCGATAGGCCTCGGGGCCACCCTGCCGGATGCGCGTCCCGATTGC 4260
      +-----+-----+-----+-----+-----+
      GCACGACTAGGCGACCGCTATCCGGAGCCCGGTGGGACGGCCTACGCGCAGGGCTAACG
4261 GCGATAGATACGCAGCGCGGCGGCGATCGACCACGCGCAGCGCGGCGGAGATGCGGAAG 4320
      +-----+-----+-----+-----+-----+
      CGCTATCTATGCGTCGCGCCCGCTAGCTGGTGCGCGTCGCGCCGCGCTCTACGCCTTC
4321 CCCCTGCCGCGCCGAGGCATAATAGGGCTCGGCCGCGTCAAGCAGGCGGATGATGACGGA 4380
      +-----+-----+-----+-----+-----+
      GGGGACGGCGCGGTCCGTATTATCCCGAGCCGGCGCAGTTTCGTCCGCCTACTACTGCCT
4381 ATAGAGCGCGTCCGAAGGCACCGGACCCCTCAACCGTCGCCCCCGCTCGGCCAGCCAGTC 4440
      +-----+-----+-----+-----+-----+
      TATCTCGCGCAGGCTTCCGTGGCCTGGGAGTTGGCAGCGGGGGCGGAGCCGTCCGTACG
4441 GGCAGGCAGATAGCAGCGCCCGATGGCGGCATCGTCGATCACGTGCGGAGCGATGTTTCGT 4500
      +-----+-----+-----+-----+-----+
      CCGTCCGTCTATCGTCGCGGGCTACCGCCGTAGCAGCTAGTGCAGCGCTCGCTACAAGCA
4501 CAGCTGGAACGCAAGGCCAGATCGCAGGCGCGATCCAGCACCGCATCGTCCCTGCACGCC 4560
      +-----+-----+-----+-----+-----+
      GTCGACCTTGCGTTCCGGGTCTAGCGTCCGCGCTAGGTCGTGGCGTAGCAGGACGTGCGG
4561 CATCACCCGCGCCATCATCACGCCCACGACCCCGCGACGTGGTAGGAATATTCCAGCAC 4620
      +-----+-----+-----+-----+-----+
      GTAGTGGGCGCGGTAGTAGTGCGGGTGTGGGGGCGCTGCACCATCCTTATAAGGTCGTG
4621 GTCATCCAGGCTGCGGTATTTCGCGATCCGCGACATCCATCGCGAAACCCTCGATCAGGTC 4680
      +-----+-----+-----+-----+-----+
      CAGTAGGTCCGACGCCATAAGCGCTAGGCGCTGTAGGTAGCGCTTTGGGAGCTAGTCCAG
4681 CATCGGCCAAAGGTCCGGGAAATCATGCCGCCGGGCGACCTGGCGCAGCGCCGGAAGGG 4740
      +-----+-----+-----+-----+-----+
      GTAGCCGGTTTCCAGGCCCTTTAGTACGGCGGGCCGCTGGACCGGTGCGGGCGCTTCCC
4741 CGGCGACATCGGGCCGTCTCTGTCAGCGCGGCCAGCGTGTGGCGCGCAGCGCCCCCAG 4800
      +-----+-----+-----+-----+-----+
      GCCGCTGTAGCCCGGAGGAGCACGTGCGCGCGGTGCGACAGCCGCGCGTTCGCGGGGTC
4801 CCGCGCCTGTGGGTGCGCGCCCGCCTCGGGGGCAGAACCCATCACCTGCCCGTCGATCAC 4860
      +-----+-----+-----+-----+-----+
      GGCGCGGACACCCAGCGGCGGGCGGAGCCCCCGTCTTGGGTAGTGGACGGGCAGCTAGTG
4861 GTCATCCGCATGCCTGCACCAGGCATAGAGCATGACCGTATCCTCGCGGATGCCGGGCGG 4920
      +-----+-----+-----+-----+-----+
      CAGTAGGCGTACGGACGTGGTCCGTATCTCGTACTGGCATAGGAGCGCCTACGGCCCCGC
4921 CATCAGCTTGGCCGCTGCGCGAAGCTTTGCGAACCCCTGCGCGATGGCCGCTTCGGAAGT 4980
      +-----+-----+-----+-----+-----+
      GTAGTCGAACCGGCGGACGCGCTTCGAAACGCTTGGGACGCGCTACCGGCGAAGCCTTCA
4981 CGCCGTGAGATCGGTGATGCGACGGCCAGGTCCGACAGCATGACCTGCGCCGTGGCCTTG 5040
      +-----+-----+-----+-----+-----+
      GCGGCAGTCTAGCCAGTACGCTGCCGGTCCAGGCTGTCTACTGGACGCGGCACCGGAAC

```

**FIG. 24E**

5041 GCGCTGCCAACGACACCCGGGATGCCCGCACCCGGATGCGTGCCCGCCCCACGATGTAG 5100  
-----+-----+-----+-----+-----+-----+-----+  
CGCGACGGTTGCTGTGGGCCCTACGGGCGTGGGCCTACGCACGGGCGGGGGTGTACATC

5101 AAGTTCGGGATCGCGCGGTTCGCGGTTATGCGGGCGGAACCAGGCGGATTGCGTCAGGATC 5160  
-----+-----+-----+-----+-----+-----+-----+  
TTCAAGCCCTAGCGCGCCAGCGCCAATACGCCCGCCTTGGTCCGCCTAACGCAGTCCTAG

5161 GGCTCGACCGAGAAGGCGCTGCCGTGATGGGCCGACAGTTCGGTGCTGAAATCGGCGGGG 5220  
-----+-----+-----+-----+-----+-----+-----+  
CCGAGCTGGCTCTTCCGCGACGGCACTACCCGGCTGTCAAGCCACGACTTTAGCCGCCCC

5221 CTGAAGATGCGGCTGACGGTCAGGTGCTTGCGCAGGTGCGGGATGGCGCGGCGCTCCAGT 5280  
-----+-----+-----+-----+-----+-----+-----+  
GACTTCTACGCCGACTGCCAGTCCACGAACGCGTCCAGCCCCTACCGCGCCGCGAGGTCA

5281 TCCTCGAAGATGCGCTCGGCATAGCCCGGGCCTCGGCTTCCCAATCGACATCGGCGCGG 5340  
-----+-----+-----+-----+-----+-----+-----+  
AGGAGCTTCTACGCGAGCCGTATCGGGCCCCGAGCCGAAGGGTTAGCTGTAGCCGCGCC

5341 CCCAGATGCGGAACGGGCGCAAGGACGTAATGCGTGACATCCCCTCGGGGGCCAGGCTG 5400  
-----+-----+-----+-----+-----+-----+-----+  
GGGTCTACGCCTTGCCCGCGTTCCTGCATTACGCACCTGTAGGGAGCCCCCGGTCCGAC

5401 GGATCGGTCACGCAGGGCGAATGCAGATACATCGAGAAATCGTCCGGCAGGCGTGGCCCG 5460  
-----+-----+-----+-----+-----+-----+-----+  
CCTAGCCAGTGCGTCCCGCTTACGTCTATGTAGCTCTTTAGCAGGCCGTCCGCACCGGGC

5461 TTGAAGATCTCGTTCACCAGCCCCCTTGTAGCGGGCCGAAGATGACGCTGTGGTGGGCC 5520  
-----+-----+-----+-----+-----+-----+-----+  
AACTTCTAGAGCAAGTGGTCGGGGAACATCGCGCCCGGCTTCTACTGCGACACCACCCGG

5521 AGGTTCTCGGGGCGCTTGGACAGGCCGAAATGCAGCACGAACAGCGACATCGACCAGCGC 5580  
-----+-----+-----+-----+-----+-----+-----+  
TCCAAGAGCCCCGGAACCTGTCCGGCTTTACGTCGTGCTTGTGCTGTAGCTGGTTCGCG

5581 TGCCGGTTCAGGATCGCGGCCTTGGTGCGCCCGCGGCGGTATGGCCCAGCAGGTTCGCGA 5640  
-----+-----+-----+-----+-----+-----+-----+  
ACGGCCAAGTCTTAGCGCCGGAACACGCGGGCGCCGCCCATACCGGGTCGTCCAGCGCT

5641 TAGCTGTGCATCACGTGCGCGTTGCTGGCCACCGTATCCGCGCGCAACTGCCGCCCGTCC 5700  
-----+-----+-----+-----+-----+-----+-----+  
ATCGACACGTAGTGACGCGGCAACGACCGGTGGCATAGGCGCGGTTGACGGCGGGCAGG

5701 AGCAGCGTGACGCCCCGTGGCGCGATCGCCCTCGGTGTGATCCGCGTGACGCGGGCATTC 5760  
-----+-----+-----+-----+-----+-----+-----+  
TCGTGCGACTGCGGGCACCGCGCTAGCGGGAGCCACAGCTAGGCGCACTGCGCCCGTAAG

5761 AGCAGCAGCGTGCCGCCAAGACGCTCGAACAGGGCGACCATGCCCGCGACCAGCTGGTTG 5820  
-----+-----+-----+-----+-----+-----+-----+  
TCGTGCTGCGACGGCGGTTCTGCGAGCTTGTCCCCTGGTACGGGCGCTGGTTCGACCAAC

5821 GTGCCGCCCTTGGCGAACCAGACGCCCGCGCGCTTCCAGCGCATGGATCAGCGCATAG 5880  
-----+-----+-----+-----+-----+-----+-----+  
CACGGCGGGAACCGCTTGGTCTGCGGCGGCGCGCAAGGTGCGGTACCTAGTCGCGTATC

5881 ATCGAGCTGGTCGAAAACGGGTTCCCGCCGACCAGCAGCGTGTGGAACGAGAAGGCCTGC 5940  
-----+-----+-----+-----+-----+-----+-----+  
TAGCTCGACCAGCTTTTGCCCAAGGGCGGCTGGTTCGTCGCACACCTTGCTCTTCCGGACG

5941 CGCAGATGCGGGTCCTGGATGAAGCGCGCCACCATGCTGTGGACCGAGCGGTATGCCTGC 6000  
-----+-----+-----+-----+-----+-----+-----+  
GCGTCTACGCCAGGACCTACTTCGCGCGGTGGTACGACACCTGGCTCGCCATACGGACG

6001 AGGCGCATCAGCGCCGGCGCGGCGTTTTCAGCATCTGGCCAGCTTCAGGAAGGGCGTGGTC 6060  
-----+-----+-----+-----+-----+-----+-----+  
TCCGCGTAGTCGCGGCCGCGCCGAAGTCGTAGACCGGGTCGAAGTCCTTCCCGCACCAG

**FIG. 24F**

```

6061 CCCAGCTTCAGATACCCCTCGCGATAGACCTCCTCGGCGTAATCGTGGAAGCGGCGATAG 6120
-----+-----+-----+-----+-----+-----+-----+
GGGTCTGAAGTCTATGGGGAGCGCTATCTGGAGGAGCCGCATTAGCACCTTCGCCGCTATC

6121 CCATCGACATCGGCGGGATTGAAGGAGGCGACCTGGCGGATCAGCTCGTCGTTCGTTC 6180
-----+-----+-----+-----+-----+-----+-----+
GGTAGCTGTAGCCGCCCTAACTTCCTCCGCTGGACCGCCTAGTCGAGCAGCAGCAGCAAG

6181 ACGTATTCTGAAGCTGCGGCCGTCCGCCCATGTCAGCCGGTAGAAGGGCGAGACCGGCAGC 6240
-----+-----+-----+-----+-----+-----+-----+
TGCATAAGCTTCGACGCCGGCAGGCGGGTACAGTCGGCCATCTTCCCGCTCTGGCCGTCC

6241 AGCGTCACGTCACGCTCCATCGGTTGGCCGCTGAGGGCCACAGCTCTCGCAGGCTGTCC 6300
-----+-----+-----+-----+-----+-----+-----+
TCGAGTGCAGTGCAGGTAGCCAACCGGCGACTCCCGGGTGTGAGAGCGTCCGACAGC

6301 GGGTCGGTCACGACCGTCGGGCCCTGCATCGAAGACGTGGCCCTGATCGTTCCAGACATAG 6360
-----+-----+-----+-----+-----+-----+-----+
CCCAGCCAGTGTCTGGCAGCCCGGACGTAGCTTCTGCACCGGGACTAGCAAGGTCTGTATC

6361 GCGCGGCCCGCCGGGCTTGTCTCGGGCCCTCGACGATGGTGGTCGCGATGCCGGCCGATTGC 6420
-----+-----+-----+-----+-----+-----+-----+
CGCGCCGGCGGCCCGAACAGCGCCCGGAGCTGCTACCACCAGCGCTACGGCCGGCTAACG

6421 AGGCGGATGGCAAGCGCAAGCCCGCCGAAACCTGCGCCGATGACGATGGCGGAATCATG 6480
-----+-----+-----+-----+-----+-----+-----+
TCCGCCTACCGTTCGCGTTCGGGCGGCTTTGGACGCGGCTACTGCTACCGCCTTGAGTAC

6481 CTCTCTCCTGCAGCAGGGGGCGTTCCGGCAGGCAGCGCACGGCCTGCGACAGCGGAATGG 6540
-----+-----+-----+-----+-----+-----+-----+
GAGAGAGGACGTCTCCCCGCAAGCCCGTCCGTGCGGTGCCGGACGCTGTCTCGCCTTACC

6541 GCGGGCGTCCGGTGACGATGCGAAGCCGGTCCGCCAATGTCAGGCGCCCGGCATAGAAGC 6600
-----+-----+-----+-----+-----+-----+-----+
CGCCCGCAGGCCACTGCTACGCTTCGGCCAGCCGGTTACAGTCCGCGGGCCGTATCTTCG

6601 GCTCGATCAGCGGCTGCGGCAGGCGGTAGAACCCTGTCAGCAGGCGATAGCGACGGTCGG 6660
-----+-----+-----+-----+-----+-----+-----+
CGAGCTAGTCGCCGACGCCGTCCGCCATCTTGGCGACGTCGTCCGCTATCGCTGCCAGCC

6661 GCGGGCAGCCGCGGAACAGCATCCGGTTTCAGCAGCCGAGGAAGCGGTTCGCGATCCGCGC 6720
-----+-----+-----+-----+-----+-----+-----+
CGCCCGTCCGCGCCTTGTCTAGGCCAAGTCGTGCGGCTCCTTCGCCAGCGCTAGGCGCG

6721 GATCGATGGCCCAGCCGCGCACCGCGCGACGGGCGGACGCGGTCTGTCAGGTTCGCGCGCCG 6780
-----+-----+-----+-----+-----+-----+-----+
CTAGCTACCGGGTCGGCGCGTGGCGCGCTGCCCGCTGCCAGCAGTCCAGCGCGCGGC

6781 CGATGGCATCCGCGACCTGCGCGGCATAGGGCAGCGAATATCCGGTGACGGGTGGAACA 6840
-----+-----+-----+-----+-----+-----+-----+
GCTACCGTAGGCGCTGGACGCGCCGTATCCCGTCGCTTATAGGCCACTGCCCCACCTTGT

6841 GCCCTGCCCCCAGCCCAACCGGCACCGCCCCCTGCGCGTGGTTCGCGCCAGAAGCCTATGG 6900
-----+-----+-----+-----+-----+-----+-----+
CGGGACGGGGGTCTGGGTTGGCCGTGGCGGGGACGCGCACAGCGCGGTCTTCGGATACC

6901 CGTCATGGGCCAGCGCGATGGGCAGGATGCCCTTTTCGCGCCGCATCTCCTGCCCGGTCC 6960
-----+-----+-----+-----+-----+-----+-----+
GCAGTACCCGGTTCGCGCTACCCGTCTACGGGAAAGCGCGGCTAGAGGACGGGCCAGG

6961 AGCCCCGCTGGCGGCATAGTCCAGCGACGCTGCGCCAGCGCGCCATCGTCCAGATCGC 7020
-----+-----+-----+-----+-----+-----+-----+
TCGGGGCGGACCGCCGTATCAGGTCTGCGGACGCGGTCTGCGCGGTAGCAGGTCTAGCG

```

**FIG. 24G**

7021 CGCCGTCGCTGTAGCGGTATCCTCGATCAGGATGCGGGTGGGACTGAAGGGCAGCAGAT 7080  
-----+-----+-----+-----+-----+-----+  
GCGGCAGCGACATCGCGCATAGGAGCTAGTCCTACGCCACCCTGACTTCCCGTCGTCTA  
7081 AGATGAAGCGGTACCCGTCCATCTGCGGAACGGTCGCGTCCATGATCATCGGGCGCTCGA 7140  
-----+-----+-----+-----+-----+-----+  
TCTACTTCGCCATGGGCAGGTAGACGCCTTGCCAGCGCAGGTACTAGTAGCCCGCGAGCT  
7141 CGCCATGGGGGGCGTCGGTCTCGATCTCGACGCCCACGAATTTCTGGAACCCACGGTCA 7200  
-----+-----+-----+-----+-----+-----+  
GCGGTACCCCCCGCAGCCAGAGCTAGAGCTGCGGGTGCTTAAAGACCTTTGGGTGCCAGT  
7201 GGTGCGGGGTCTCGACGGCACCACGGGCGTCGATCACGCAGGCAGCCTCGATCCGCGAGC 7260  
-----+-----+-----+-----+-----+-----+  
CCACGCCCCAGAGCTGCCGTGGTGCCCGCAGCTAGTGCGTCCGTCGGAGCTAGGCGCTCG  
7261 CGTCCGTCAGCGTCGCGCCGGTATCGTCCAGCGTCGCGACATGCGTATTCACCCGAGAT 7320  
-----+-----+-----+-----+-----+-----+  
GCAGGCAGTCGCAGCGCGGCCATAGCAGGTGCGAGCGCTGTACGCATAAGGTGGCGTCTA  
7321 CGACACCCTGCAGCAGCCCCGATCAGCGCGCCCGCCTCGATCGAGCCATAGCCTGTCTGTC 7380  
-----+-----+-----+-----+-----+-----+  
GCTGTGGGACGTCTGTCGGGCTAGTCGCGCGGGCGGAGCTAGCTCGGTATCGGACAGCAGT  
7381 GCGCGCGCGAATGGTCGGGAAACGCGACCTCCTGATCCGTCCATTCGCCGCGACGAATGG 7440  
-----+-----+-----+-----+-----+-----+  
CCGCCGCGCTTACCAGCCCTTTGCGCTGGAGGACTAGGCAGGTAAGCGGCGCTGCTTACC  
7441 GCGACAGGCGCGCCAGCCATTCGGGCGAAAGATCCGTGTCTGTCGGCAGGACCAGGTGTGCT 7500  
-----+-----+-----+-----+-----+-----+  
CGCTGTCCGCGCGGTTCGGTAAGCCCGCTTTCTAGGCACAGCACCGTCTTGGTCCACACGA  
7501 GGTCCGAGGGGCCGGACCGCGCGTCGAGCATCACGATGCGCGCATCCGGTCTGCGGTGCGC 7560  
-----+-----+-----+-----+-----+-----+  
CCAGGCTCCCCGGCCTGGCGCGCAGCTCGTAGTGCTACGCGCTAGGCCAGACGCCAGCG  
7561 GAACGGCAAGCGCGATCAGCGCACCGGACAGCCCCGCGCCGCGATCAGCAGATCATGGC 7620  
-----+-----+-----+-----+-----+-----+  
CTTGCCGTTTCGCGCTAGTCGCGTGGCCTGTTCGGGGCGGGGCGCTAGTCGTCTAGTACCG  
7621 TCATGTATTGCGATCCGCCCCCTTCGCGGTCTTTCAGCAGCGCGCCCGAGCGTTTCAGCTC 7680  
-----+-----+-----+-----+-----+-----+  
AGTACATAACGCTAGGCGGGGAAGCGCCAGGAAGTCGTGCGCGGGGCTCGCAAAGTCGAG  
7681 TGCCTTGAGGCTGTGACCGAGGGCGCCAGATGAAACCGAAGCTGACGCAGTTCTCGCG 7740  
-----+-----+-----+-----+-----+-----+  
ACGGAACCTCCGACAGCTGGCTCCCGCGGGTCTACTTTGGCTTCGACTGCGTCAAGAGCGC  
7741 GCCATGGACCGGTGATGCATCCTGTGTGCCTGGTAGACGCGACGAAGATAGCCGCGCTT 7800  
-----+-----+-----+-----+-----+-----+  
CGGTACCTGGCGCACTACGTAGGACACACGGACCATCTGCGCTGCTTCTATCGGCGCGAA  
7801 GGGGACATAGCGGAACGGCCAGCGCCCATGCACCAAGCCGTCATGCAGGAAATAGTAGAT 7860  
-----+-----+-----+-----+-----+-----+  
CCCCTGTATCGCCTTGCCGGTCGCGGGTACGTGGTTCGGCAGTACGTCTTTATCATCTA  
7861 CAGCCCGTAGCAGGTGACCCCCACCGCCAGCCACCAGGCCAGATCCGACCCCATCGCGCC 7920  
-----+-----+-----+-----+-----+-----+  
GTCGGGCATCGTCCACTGGGGGTGGCGGTGGTGGTCCGGTCTAGGCTGGGGTAGCGCGG  
7921 GATCGCGAACAGCAGATCGAGATTACCGCGAAGATGACGCCATAGAGGTCGTTCTTCTC 7980  
-----+-----+-----+-----+-----+-----+  
CTAGCGCTTGTCGTGCTAGCTCTAATGGCGCTTCTACTGCGGTATCTCCAGCAAGAAGAG

FIG. 24H

```

7981 GAGCGCGTGGTTCGTGATCCTCGTCGTGGTGCGATTTATGCCAGCCCCAGCCCAGGGGGCC 8040
      +-----+-----+-----+-----+-----+-----+
      CTCGCGCACCAGCACTAGGAGCAGCACCACGCTAAATACGGTCGGGGTCGGGTCCCCCGG

8041 ATGCATGATCCACCGATGGACGGAGTAGGCCGTGAGCTCCATCGCGGCAGCGGTGAGGAT 8100
      +-----+-----+-----+-----+-----+-----+
      TACGTACTAGGTGGCTACCTGCCTCATCCGGCAGTCGAGGTAGCGCCGCTGCCAGTCCTA

8101 GACGGTCAGGATTGCGGGCCCAAGTGCTCATGCCGGCCCCCTTGCTTGATATGACAGGGAAC 8160
      +-----+-----+-----+-----+-----+-----+
      CTGCCAGTCCTAACGCCGGGTTACAGAGTACGGCCGGGGAACGAACTATACTGTCCCTTG

8161 AGGCTACGCTGCCGCGCGGTGCATGACCAGCCCATCGGGGTGCGACCAAAGGGCATCGCG 8220
      +-----+-----+-----+-----+-----+-----+
      TCCGATGCGACGGCGCGCCACGTACTGGTCGGGTAGCCCCACGCTGGTTTCCCGTAGCGC

8221 TGACATCTGCGTTCAGGGCTCATAGCGGGATCATCCGTGACATTCGCCGCCGAACGCGGC 8280
      +-----+-----+-----+-----+-----+-----+
      ACTGTAGACGCAAGTCCCGAGTATCCGCCTAGTAGGCACTGTAAGCGGCGGCTTGCGCCG

8281 AGGCGCATCACGCGTTCCGTCGCTGGAAATATTAATGTTTTCCCGAAGATGGTCGGGGCG 8340
      +-----+-----+-----+-----+-----+-----+
      TCCGCGTAGTGCGCAAGGCAGCGACCTTTATAATTACAAAAGGGCTTCTACCAGCCCCGC

8341 AGAGGATTGCAACCTCCGACCTACGGTACCCAAAACCGTCGCGCTACCAGGCTGCGCTAC 8400
      +-----+-----+-----+-----+-----+-----+
      TCTCCTAAGCTTGGAGGCTGGATGCCATGGGTTTTGGCAGCGCGATGGTCCGACGCGATG

8401 GCCCCGACTGCGGAAGGCTTTAGCCGATTGTTCCGGCAAGGGAAAGACCTAGTCGCAGGC 8460
      +-----+-----+-----+-----+-----+-----+
      CGGGGCTGACGCCTTCCGAAATCGGCTAACAAGGCCGTTCCCTTTCTGGATCAGCGTCCG

8461 CAGGACCGCATTTGTCGCCCATGCCCGGATGCGCCATCGGCTGACCGGGCTTCAGGCCAAG 8520
      +-----+-----+-----+-----+-----+-----+
      GTCCGTGGCGTAACAGCGGGTACGGGCCTACGCGGTAGCCGACTGGCCCCAAGTCCGGTTC

8521 GCGATCCGCCTCTCCGCCCCGCGATTTGAGGACGAACAGCCGGTCGGGGTCCGGATCGCC 8580
      +-----+-----+-----+-----+-----+-----+
      CGCTAGGCGGAGAGCGGGCGCTAAAGCTCCTGCTTGTGCGCCAGCCCCAGGCCTAGCGG

8581 GACCGCCGCGCCCGAATGGGCGTCTCGTCCAGCGGGCGCGCATTGCGGTGGATGTGGCG 8640
      +-----+-----+-----+-----+-----+-----+
      CTGGCGGCGGGGCTTACCCGAGAGCAGGTGCGCCGCGCGTAACGCCACCTACACCGC

8641 GATGACGCGGTTTTCATCCGCAAAGACCATGTCCAGCGGGATCAGTGTGTTGCGCATCCA 8700
      +-----+-----+-----+-----+-----+-----+
      CTACTGCGGCCAAAGTAGGCGTTTCTGGTACAGGTGCGCCCTAGTCACACAACGCGTAGGT

8701 GAAGGACACCGGCTGGGGCGATTGCTAGATGAACAGCATTCGGGTGCCCGCAGGCAGCTC 8760
      +-----+-----+-----+-----+-----+-----+
      CTTCTGTGGCCGACCCCGCTAAGCATCTACTTGTGCGTAAGGCCACGGGCGTCCGTCGAG

8761 CTTGCGGAACATCAGGCCCTGCGCGCGCTCTTCGGGGCTGTCCGCGACCTCGACCCGAAA 8820
      +-----+-----+-----+-----+-----+-----+
      GAACGCCTTGTAGTCCGGGACGCGCGGAGAAGCCCCGACAGGCGCTGGAGCTGGGCTTT

8821 CCCGAGCGTTTCCGCACCGGTATCGACGACAAGACTGCCGGGCGCGCATTCACCCGCCG 8880
      +-----+-----+-----+-----+-----+-----+
      GGGCTCGCAAAGGCGTGGCCATAGCTGCTGTTCTGACGGCCCCGCGTAAGGTGGCGGCG

8881 CGCGGGCGGGCATCAGGACCGCAAGAAGCGCTGCGGCCCTTACTCGGCCACATGGGCAA 8940
      +-----+-----+-----+-----+-----+-----+
      GCGCCGCCGCCCGTAGTCCTGGCGTTCTTCGCGACGCGCGAATGAGCCGGTGTACCCGTT

8941 GATAGGACTGCTCGGCGCCGAGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCG 9000
      +-----+-----+-----+-----+-----+-----+
      CTATCCTGACGAGCCGCGGCTCTAGGGGGCCCCGACGTCCTTAAGCTATAGTTTCAATAGC

```

**FIG. 24I**

```

9001 ATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCTTTAGTGAGGGTTA
-----+-----+-----+-----+-----+-----+-----+
9060 TATGGCAGCTGGAGCTCCCCCGGGCCATGGGTGAAAACAAGGGAAATCACTCCCAAT
-----+-----+-----+-----+-----+-----+-----+

9061 ATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC
-----+-----+-----+-----+-----+-----+-----+
9120 TAACGCGCGAACC GCATTAGTACCAGTATCGACAAAGGACACACTTTAACAATAGGCGAG
-----+-----+-----+-----+-----+-----+-----+

9121 ACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCTAATGA
-----+-----+-----+-----+-----+-----+-----+
9180 TGTTAAGGTGTGTTGTATGCTCGGCCTTCGTATTTACATTTTCGGACCCACGGATTACT
-----+-----+-----+-----+-----+-----+-----+

9181 GTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGCTTTCAGTCGGGAAACCTG
-----+-----+-----+-----+-----+-----+-----+
9240 CACTCGATTGAGTGTAAATTAACGCAACGCGAGTGACGGCGAAAGGTCAGCCCTTTGGAC
-----+-----+-----+-----+-----+-----+-----+

9241 TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGG
-----+-----+-----+-----+-----+-----+-----+
9300 AGCACGGTCGACGTAATTACTTAGCCGGTTGCGCGCCCTCTCGCCAAACGCATAACCC
-----+-----+-----+-----+-----+-----+-----+

9301 CGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCTGCGGCGAGCG
-----+-----+-----+-----+-----+-----+-----+
9360 GCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACCGCGCTCGC
-----+-----+-----+-----+-----+-----+-----+

9361 GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGA
-----+-----+-----+-----+-----+-----+-----+
9420 CATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCT
-----+-----+-----+-----+-----+-----+-----+

9421 AAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
9480 TTCTTGTA CACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTTTCCGGCGCAACGAC
-----+-----+-----+-----+-----+-----+-----+

9481 GCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG
-----+-----+-----+-----+-----+-----+-----+
9540 CGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTTCAGTC
-----+-----+-----+-----+-----+-----+-----+

9541 AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC
-----+-----+-----+-----+-----+-----+-----+
9600 TCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAG
-----+-----+-----+-----+-----+-----+-----+

9601 GTGCGCTCTCCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG
-----+-----+-----+-----+-----+-----+-----+
9660 CACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGC
-----+-----+-----+-----+-----+-----+-----+

9661 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT
-----+-----+-----+-----+-----+-----+-----+
9720 CCTTCGCACCGCGAAAGAGTATCGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAA
-----+-----+-----+-----+-----+-----+-----+

9721 CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTAGCCCCGACCGCTGCGCCTTATCC
-----+-----+-----+-----+-----+-----+-----+
9780 GCGAGGTTGACCCGACACAGTGCTTGGGGGCAAGTCGGGCTGGCGACGCGGAATAGG
-----+-----+-----+-----+-----+-----+-----+

9781 GGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC
-----+-----+-----+-----+-----+-----+-----+
9840 CCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGG
-----+-----+-----+-----+-----+-----+-----+

9841 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
-----+-----+-----+-----+-----+-----+-----+
9900 TGACCATTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACC
-----+-----+-----+-----+-----+-----+-----+

9901 TGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA
-----+-----+-----+-----+-----+-----+-----+
9960 ACCGGATTGATGCCGATGTGATCTTCCTGTCTATAAACCATAGACGCGAGACGACTTCGGT
-----+-----+-----+-----+-----+-----+-----+

```

**FIG. 24J**

```

9961 GTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC 10020
-----+-----+-----+-----+-----+-----+-----+
CAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGTTGGTGGCGACCATCG

10021 GGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT 10080
-----+-----+-----+-----+-----+-----+-----+
CCACCAAAAAACAAACGTTGTCGTCCTAATGCGCGTCTTTTTTTCCTAGAGTTCTTCTA

10081 CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATT 10140
-----+-----+-----+-----+-----+-----+-----+
GGAAACTAGAAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCTTAA

10141 TTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT 10200
-----+-----+-----+-----+-----+-----+-----+
AACCAGTACTCTAATAGTTTTTCTAGAAGTGGATCTAGGAAAATTTAATTTTACTTCA

10201 TTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATC 10260
-----+-----+-----+-----+-----+-----+-----+
AAATTTAGTTAGATTTTATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAG

10261 AGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCC 10320
-----+-----+-----+-----+-----+-----+-----+
TCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGG

10321 GTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA 10380
-----+-----+-----+-----+-----+-----+-----+
CAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGTCACGACGTTACTAT

10381 CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGG 10440
-----+-----+-----+-----+-----+-----+-----+
GGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTGGTTCGGCCTTCC

10441 GCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGC 10500
-----+-----+-----+-----+-----+-----+-----+
CGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACG

10501 CGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCT 10560
-----+-----+-----+-----+-----+-----+-----+
GCCCTTCGATCTCATTCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGA

10561 ACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAA 10620
-----+-----+-----+-----+-----+-----+-----+
TGTCCGTAGCACCACAGTGGCAGCAGCAAACCATAACGAAGTAAGTCGAGGCCAAGGGTT

10621 CGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGT 10680
-----+-----+-----+-----+-----+-----+-----+
GCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCA

10681 CCTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCA 10740
-----+-----+-----+-----+-----+-----+-----+
GGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGT

10741 CTGCATAATTCTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTAC 10800
-----+-----+-----+-----+-----+-----+-----+
GACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATG

10801 TCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCA 10860
-----+-----+-----+-----+-----+-----+-----+
AGTTGGTTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGAGT

10861 ATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGT 10920
-----+-----+-----+-----+-----+-----+-----+
TATGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGCA

10921 TCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTGATGTAACCC 10980
-----+-----+-----+-----+-----+-----+-----+
AGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGG

```

**FIG. 24K**

```
10981 ACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCA 11040
-----+-----+-----+-----+-----+-----+
TGAGCACGTGGGTTGACTAGAAAGTCGTAGAAAATGAAAGTGGTCGCAAAGACCCACTCGT
11041 AAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATA 11100
-----+-----+-----+-----+-----+-----+
TTTTGTCCTTCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAATTAT
11101 CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGC 11160
-----+-----+-----+-----+-----+-----+
GAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCG
11161 GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCGCACATTTCCC 11220
-----+-----+-----+-----+-----+-----+
CCTATGTATAAACTTACATAAATCTTTTATTGTTTATCCCAAGGCGCGTGTAAGGG
11221 CGAAAAGTGCCAC
-----+----- 11233
GCTTTTCACGGTG
```

FIG. 24L



FIG. 25A

[illegible]

FIG. 25B

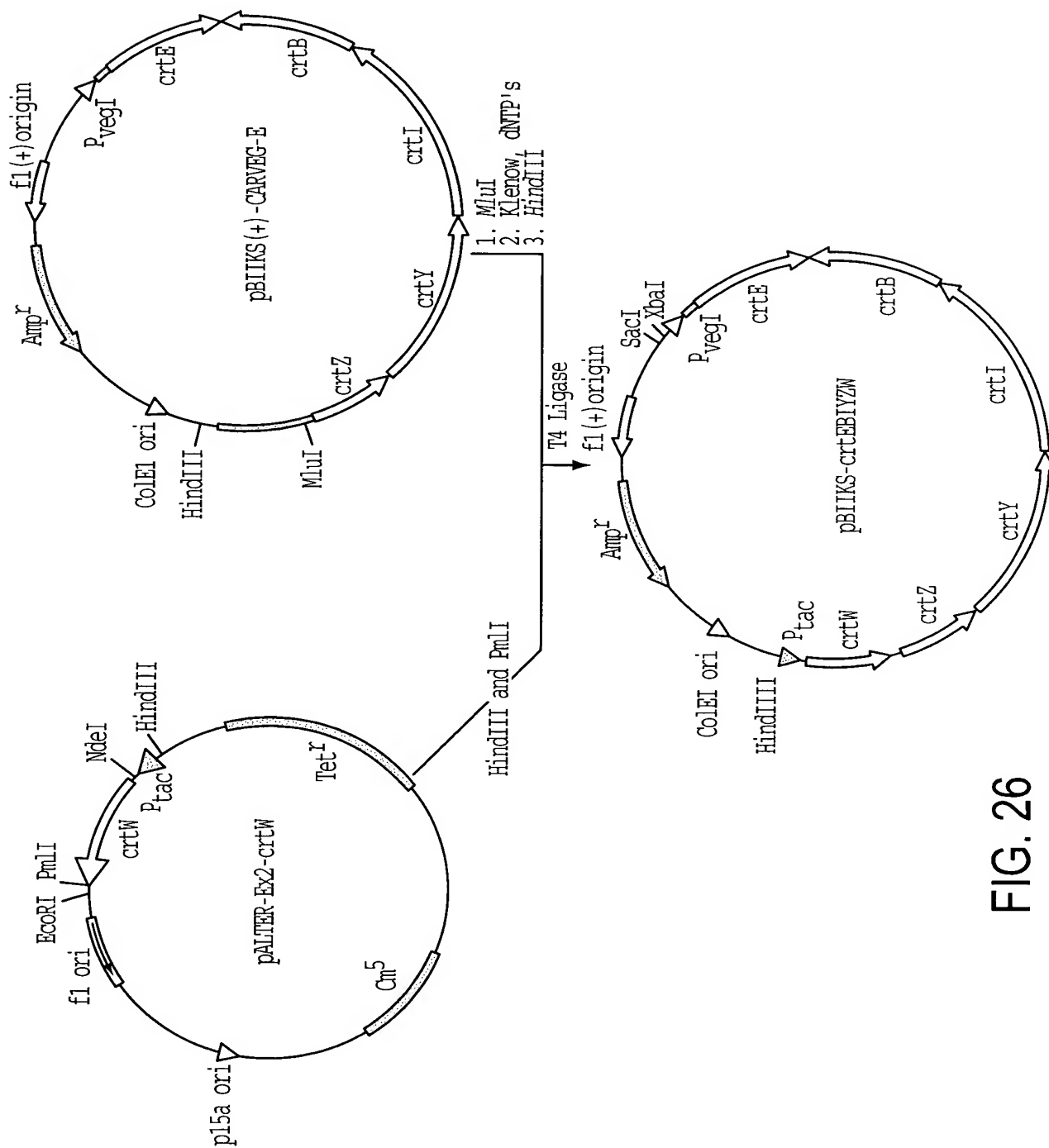


FIG. 26

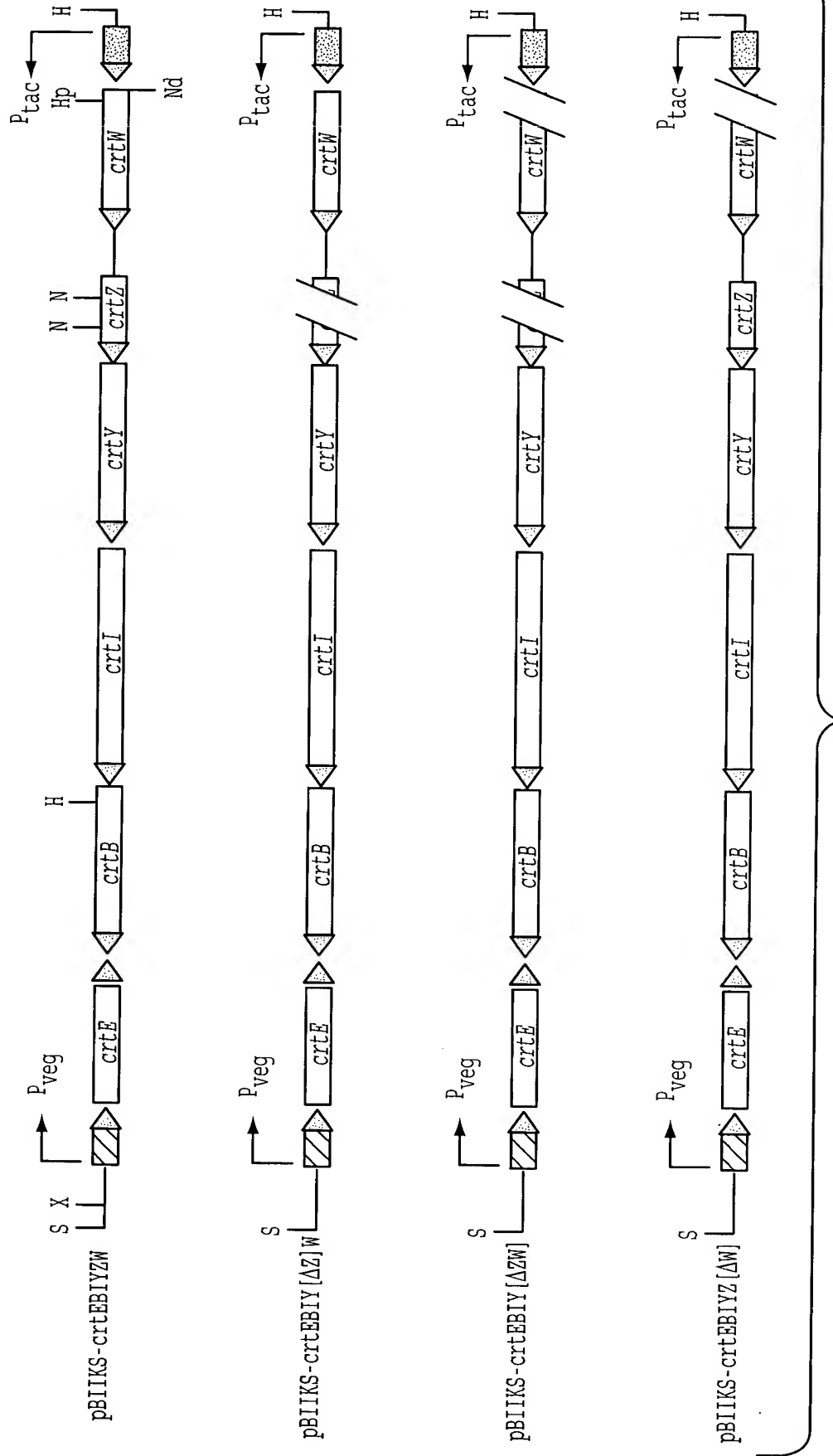


FIG. 27

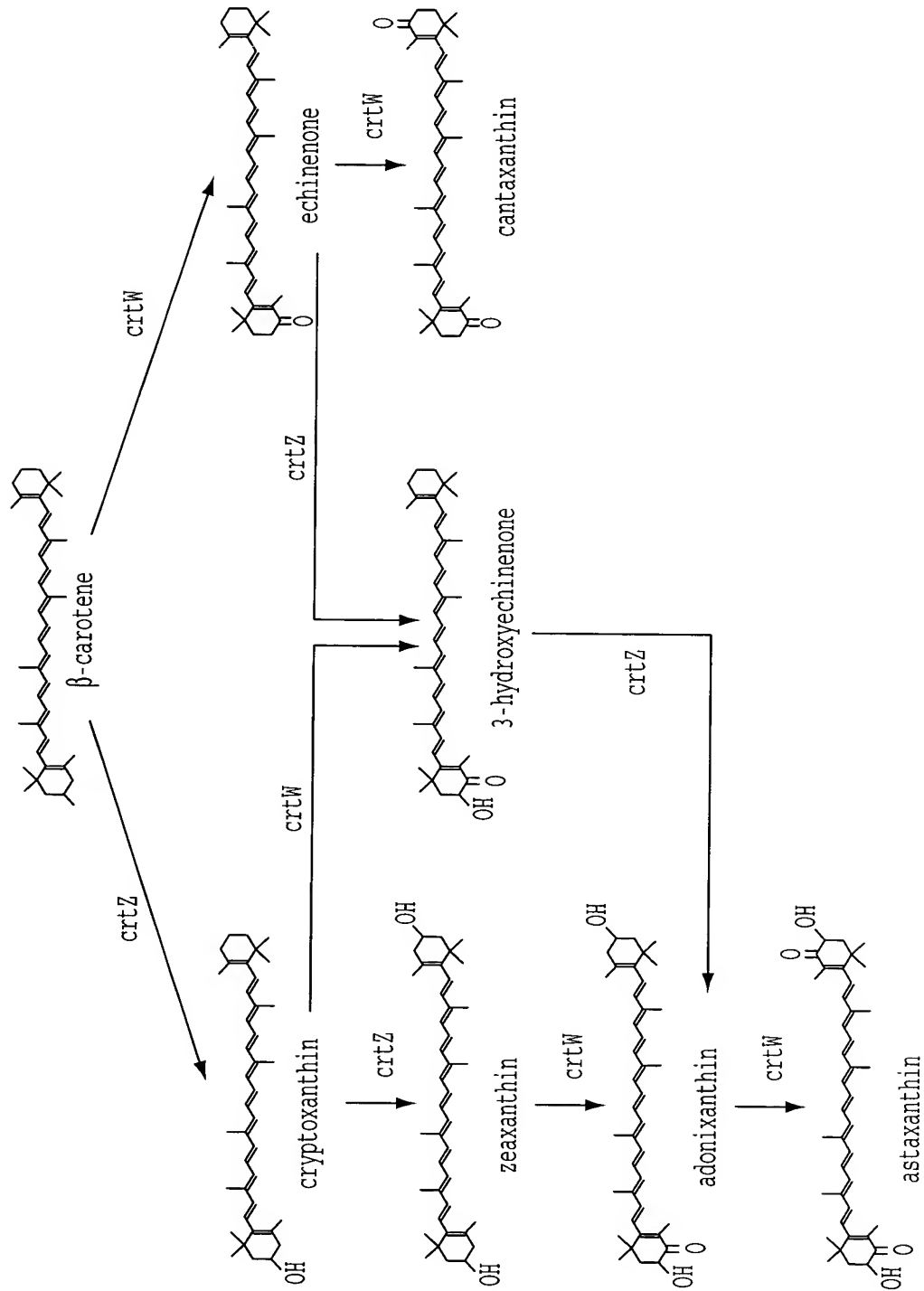


FIG. 28

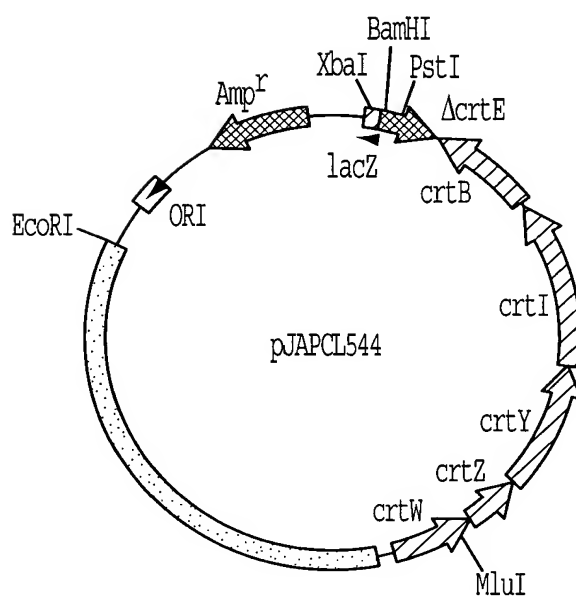


FIG. 29

```

1  ACTGTAGTCTGCGCGGATCGCCGGTCCGGGGGACAAGATATGAGCGCACATGCCCTGCCC
   -----+-----+-----+-----+-----+-----+
61  TGACATCAGACGCGCCTAGCGGCCAGGCCCCCTGTTCTATACTCGCGTGTACGGGACGGG
   -----+-----+-----+-----+-----+-----+
   AAGGCAGATCTGACCGCCACCAGTTTGATCGTCTCGGGCGGCATCATCGCCGCGTGGCTG
61  -----+-----+-----+-----+-----+-----+
   TTCCGTCTAGACTGGCGGTGGTCAAACCTAGCAGAGCCCCCGCTAGTAGCGGCGCACCGAC
   -----+-----+-----+-----+-----+-----+
121  GCCCTGCATGTGCATGCGCTGTGGTTTCTGGACGCGGCGGCATCCCATCCTGGCGGTC
   -----+-----+-----+-----+-----+-----+
   CGGGACGTACACGTACGCGACACCAAAGACCTGCGCCGCCGCTAGGGTAGGACCGCCAG
   -----+-----+-----+-----+-----+-----+
181  GCGAATTTCTGGGGCTGACCTGGCTGTGGTCTGGTCTGTTTCATCATCGCGCATGACGCG
   -----+-----+-----+-----+-----+-----+
   CGCTTAAAGGACCCCCGACTGGACCGACAGCCAGCCAGACAAGTAGTAGCGCGTACTGCGC
   -----+-----+-----+-----+-----+-----+
241  ATGCATGGGTTCGGTTCGTGCCGGGGCGCCCGCGCGCAATGCGGCGATGGGCCAGCTTGTC
   -----+-----+-----+-----+-----+-----+
   TACGTACCCAGCCAGCACGGCCCCGCGGGCGCGGGTTACGCCGCTACCCGGTCAACAG
   -----+-----+-----+-----+-----+-----+
301  CTGTGGCTGTATGCCGGATTTTCTGGCGCAAGATGATCGTCAAGCACATGGCCCATCAT
   -----+-----+-----+-----+-----+-----+
   GACACCGACATACGGCCTAAAAGGACCGCGTTCTACTAGCAGTTCGTGTACCGGGTAGTA
   -----+-----+-----+-----+-----+-----+
361  CGCCATGCCGGAACCGACGACGACCCAGATTTGACCATGGCGGCCCCGGTCCGCTGGTAC
   -----+-----+-----+-----+-----+-----+
   GCGGTACGGCCTTGGCTGCTGCTGGGTCTAAAGCTGGTACCGCCGGGCCAGGCGACCATG
   -----+-----+-----+-----+-----+-----+
421  GCCCCGTTTCATCGGCACCTATTTCTGGCTGGCGCGAGGGGCTGCTGCTGCCCCGTCATCGTG
   -----+-----+-----+-----+-----+-----+
   CGGGCGAAGTAGCCGTGGATAAAGCCGACCGCGCTCCCCGACGACGAGGGCAGTAGCAC
   -----+-----+-----+-----+-----+-----+
481  ACGGTCTATGCGCTGATGTTGGGGGATCGCTGGATGTACGTGGTCTTCTGGCCGTTGCCG
   -----+-----+-----+-----+-----+-----+
   TGCCAGATACGCGACTACAACCCCTAGCGACCTACATGCACCAGAAGACCGGCAACGGC
   -----+-----+-----+-----+-----+-----+
541  TCGATCCTGGCGTCGATCCAGCTGTTTCGTGTTTCGGCATCTGGCTGCCGCACCGCCCCGGC
   -----+-----+-----+-----+-----+-----+
   AGCTAGGACCGCAGCTAGGTCGACAAGCACAAGCCGTAGACCGACGGCGTGGCGGGGCCG
   -----+-----+-----+-----+-----+-----+
601  CACGACGCGTTCCCGGACCGCCACAATGCGCGGTCTGTCGCGGATCAGCGACCCCGTGTCG
   -----+-----+-----+-----+-----+-----+
   GTGCTGCGCAAGGGCCTGGCGGTGTTACGCGCCAGCAGCGCCTAGTCGCTGGGGCACAGC
   -----+-----+-----+-----+-----+-----+

```

**FIG. 30A**

661	CTGCTGACCTGCTTTCACTTTGGCGGTTATCATCACGAACACCACCTGCACCCGACGGTG -----+-----+-----+-----+-----+-----+-----+ GACGACTGGACGAAAGTGAAACCGCCAATAGTAGTGCTTGTGGTGGACGTGGGCTGCCAC	720
721	CCTTGGTGGCGCCTGCCCAGCACCCGCACCAAGGGGGACACCGCATGACCAATTTCTCTGA -----+-----+-----+-----+-----+-----+-----+ GGAACCACCGCGGACGGGTCTGTTGGCGTGGTTCCCCCTGTGGCGTACTGGTTAAAGGACT	780
781	TCGTCGTCGCCACCGTGCTGGTGTATGGAGCTGACGGCCTATTCCGTCCACCGCTGGATCA -----+-----+-----+-----+-----+-----+-----+ AGCAGCAGCGGTGGCAGCACTACCTCGACTGCCGGATAAGGCAGGTGGCGACCTAGT	840
841	TGCACGGCCCCCTTGGGCTGGGGCTGGCACAAGTCCCACCACGAGGAACACGACCACGCGC -----+-----+-----+-----+-----+-----+-----+ ACGTGCCGGGGAACCCGACCCGACCGTGTTTCAAGGTGGTGCTCCTTGTGCTGGTGCGCG	900
901	TGGAAAAGAACGACCTGTACGGCCTGGTCTTTGCGGTGATCGCCACGGTGCTGTTTACGG -----+-----+-----+-----+-----+-----+-----+ ACCTTTTCTTGCTGGACATGCCGGACCAGAAACGCCACTAGCGGTGCCACGACAAGTGCC	960
961	TGGGCTGGATCTGGGCACCGGTCTGTGGTGGATCGCCTTGGGCATGACCGTCTACGGGC -----+-----+-----+-----+-----+-----+-----+ ACCCGACCTAGACCCGTGGCCAGGACACCACCTAGCGGAACCCGTACTGGCAGATGCCCCG	1020
1021	TGATCTATTTTCGTCTGCATGACGGGCTGGTGCATCAGCGCTGGCCGTTCCGCTATATCC -----+-----+-----+-----+-----+-----+-----+ ACTAGATAAAGCAGGACGTACTGCCCCACCACGTAGTCGCGACCGGCAAGGCGATATAGG	1080
1081	CTCGCAAGGGCTATGCCAGACGCCTGTATCAGGCCCACCGCCTGCACCACGCGGTGAGG -----+-----+-----+-----+-----+-----+-----+ GAGCGTTCCCGATACGGTCTGCGGACATAGTCCGGGTGGCGGACGTGGTGCGCCAGCTCC	1140
1141	GGCGCGACCATTGCGTCAGCTTCGGCTTCATCTATGCGCCGCCGGTCGACAAGCTGAAGC -----+-----+-----+-----+-----+-----+-----+ CCGCGCTGGTAACGCAGTCGAAGCCGAAGTAGATACGCGCGGCCAGCTGTTGCACTTCG	1200
1201	AGGACCTGAAGACGTGCGGCGTGCTGCGGGCCGAGGCGCAGGAGCGCACGTGACCCATGA -----+-----+-----+-----+-----+-----+-----+ TCCTGGACTTCTGCAGCCCGCACGACGCCCGGCTCCGCGTCCTCGCGTGCACTGGGTACT	1260
1261	C - 1261 G	

**FIG. 30B**





Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MSAHALPKAD LTATSLIVSG GIIAAWLALH VHALWFLDAA AHPILAVANF  
51 LGLTWLSVGL FIIAHDAMHG SVVPGRPRAN AAMGQLVLWL YAGFSWRKMI  
101 VKHMAHHRHA GTDDDPDFDH GGPVRWYARF IGTYFGWREG LLLPVIVTVY  
151 ALMLGDRWMY VVFWPLPSIL ASIQLFVFGI WLPHRPGHDA FPDRHNARSS  
201 RISDPVSLLT CFHFGGYHHE HHLHPTVPWW RLPSTRTKGD TA\*

**FIG. 32**

```

1  ATGACCAATTTCTGATCGTCGTCGCCACCGTGCTGGTGATGGAGCTGACGGCCTATTCC      60
   -----+-----+-----+-----+-----+-----+
TACTGGTTAAAGGACTAGCAGCAGCGGTGGCAGCACCCTACCTCGACTGCCGGATAAGG

61  GTCCACCGCTGGATCATGCACGGCCCCCTTGGGCTGGGGCTGGCACAAGTCCCACCACGAG      120
   -----+-----+-----+-----+-----+-----+
CAGGTGGCGACCTAGTACGTGCCGGGGAACCCGACCCCGACCGTGTTCAAGGTGGTGCTC

121  GAACACGACCACGCGCTGGAAAAGAACGACCTGTACGGCCTGGTCTTTGCGGTGATCGCC      180
   -----+-----+-----+-----+-----+-----+
CTTGTGCTGGTGCGCGACCTTTTCTTGCTGGACATGCCGGACCAGAAACGCCACTAGCGG

181  ACGGTGCTGTTACGGTGGGCTGGATCTGGGCACCGGTCCTGTGGTGGATCGCCTTGGGC      240
   -----+-----+-----+-----+-----+-----+
TGCCACGACAAGTGCCACCCGACCTAGACCCGTGGCCAGGACACCACCTAGCGGAACCCG

241  ATGACCGTCTACGGGCTGATCTATTTCTGCTCATGACGGGCTGGTGATCAGCGCTGG      300
   -----+-----+-----+-----+-----+-----+
TACTGGCAGATGCCCAGCTAGATAAAGCAGGACGTACTGCCCAGCACGTAGTCGCGACC

301  CCGTTCCGCTATATCCCTCGCAAGGGCTATGCCAGACGCCTGTATCAGGCCCACCGCCTG      360
   -----+-----+-----+-----+-----+-----+
GGCAAGGCGATATAGGGAGCGTTCCCGATACGGTCTGCGGACATAGTCCGGGTGGCGGAC

361  CACCACGCGGTCGAGGGGCGCGACCATTGCGTCAGCTTCGGCTTCATCTATGCGCCGCCG      420
   -----+-----+-----+-----+-----+-----+
GTGGTGCGCCAGCTCCCCGCGCTGGTAACGCAGTCAAGCCGAAGTAGATACGCGGCGGC

421  GTCGACAAGCTGAAGCAGGACCTGAAGACGTGCGGGCTGCTGCGGGCCGAGGCGCAGGAG      480
   -----+-----+-----+-----+-----+-----+
CAGCTGTTTCGACTTCGTCTGGACTTCTGCAGCCCGCACGACGCGCGGCTCCGCGTCCTC

CGCACG
481  ----- 486
GCGTGC

```

**FIG. 33**

Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MTNFLIVVAT VLMELTAYS VHRWIMHGPL GWGWHKSHHE EHDHALEKND  
51 LYGLVFAVIA TVLFTVGWIW APVLWWIALG MTVYGLIYFV LHDGLVHQRW  
101 PFRYIPRKG Y ARRLYQAHRL HHAVEGRDHC VSFGFIYAPP VDKLKQDLKT  
151 SGVLRAEAQE RT

**FIG. 34**

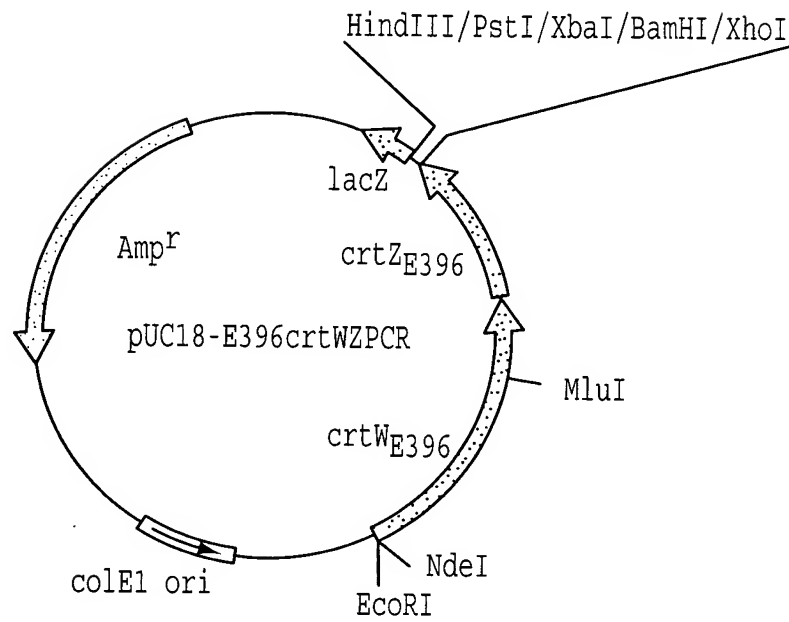


FIG. 35

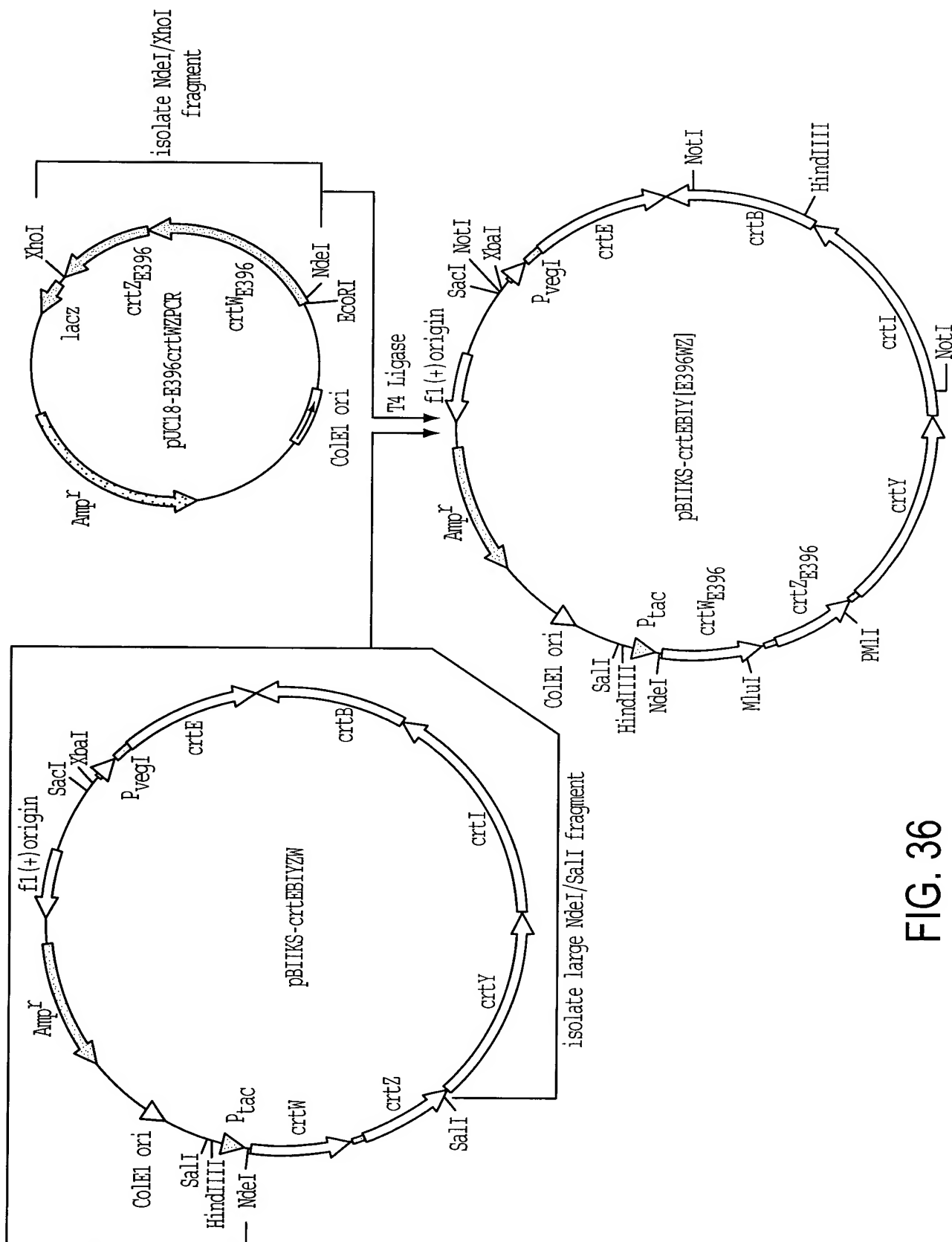


FIG. 36



FIG. 37

1	CTGCAGGTCTGACACGGCCAGAAGGCCGCGCCGGGGcCGGGGGCCGcGCATCGCGACC -----+-----+-----+-----+-----+-----+-----+ GACGTCCAGACTGTGCCGGTCTTCCGGCGCGGCGCCcgCCCCCGGCGgCGTAGCGCTGG	60
61	GGTATCCTTGCCAAGCGCCGCTGGTCGCCCCACaACGTCCAGCAGGTCGTCATAGGACTG -----+-----+-----+-----+-----+-----+-----+ CCATAGGAACGGTTCGCGGCGGACCAGCGGGTgtTGCAGGTCGTCCAGCAGTATCCTGAC	120
121	GAACACCCGGCCCAGCTGACGGCCAAAGTCGATCATCTGaGTCTGCTCCTCGGCGTCGAA -----+-----+-----+-----+-----+-----+-----+ CTTGTGGCCGGGTCGACTGCCGGTTTCAGCTAGTAGACtCAGACGAGGAGCCGCAGCTT	180
181	CTCCTTGATCACGGCCAGCATCTCCAGCCCGGCGATGAACAGCACGCCGGTCTTCAGGTC -----+-----+-----+-----+-----+-----+-----+ GAGGAACtAGTGCCGGTCGTAGAGGTCGGGCCGCTACTTGTCTGTCGGCCAGAAGTCCAG	240
241	CTGTTCTGTTCGACCCCCGCGCCGTCTTGGCCGCGTGCAGGTCCAGGTCCTGGCCGGC -----+-----+-----+-----+-----+-----+-----+ GACAAGGACAAGCTGGGGGCGCGGCAAGAACCGGCGCACGTCCAGGTCCAGGACCGGCCG	300
301	GCACAGGCCCTGCGGCCCCAGGGACCGGACAGGATCCgcaccagctgcgcccgcaccgt -----+-----+-----+-----+-----+-----+-----+ CGTGTCCGGGACGCGGGGTCCCTGGCGCTGTCTAGGcgtggtcgacgcgggcgtggca	360
361	gcccgcgcgcgcgcgcaccggccagcagggccatcgctcggtgatcagggcgatgcc -----+-----+-----+-----+-----+-----+-----+ cgggctgcgcggcgcgcggtggccggtcgtcccggtagcggagccactagtcccgtacgg	420
421	gcctagcacggcgcggtttcgccatgcgccacatgggtcgcgggctggccgcggcgag -----+-----+-----+-----+-----+-----+-----+ cggatcgtgccgcgcgaaagcggtacgcggtgtaccagcgcccagccggcgccgcgtc	480
481	cccggcatcgtccatgcagggcaggtcgtcgaagatcagcgatgcggcatgcaccatctc -----+-----+-----+-----+-----+-----+-----+ gggccgtagcaggtacgtcccgtccagcagcttctagtgcgtacgccgtacgtggtagag	540
541	gaccgcgcagggcggtcgacgatcgtgtcgagaccccgccgaggttctgccgcaag -----+-----+-----+-----+-----+-----+-----+ ctggcgcgctccgcccagctgctagcacagcgtctggggcgggctccgaagacggcggttc	600
601	cagcatcagcatgccgcggaacgcttgcccagcacagcgcccatggctcatggccgg -----+-----+-----+-----+-----+-----+-----+ gtcgtagtcgtacggcgcccttgccaacgggctgctgtcgcgcggtaccgagtaccggcc	660
661	gccgagcggctgcgacacggcaccgaatccctgggcgatctcctcaagtctggtctgcag -----+-----+-----+-----+-----+-----+-----+ cggctcgccgacgctgtgccgtggcttagggacccgctagaggagttcagaccagacgtc	720

**FIG. 38A**



721	aaggggtggcgtggatcgggttgacgtctcgtctcatcagtcgcttcgcgcttgggttctg -----+-----+-----+-----+-----+-----+-----+ ttcccaccgcacctaggggaactgcagagcagagtagtcacggaagcggaacccaagac	780
781	accaggcggaaggtcaggccggggcgccacccgtgacccgtcatccaccgtcaacagt -----+-----+-----+-----+-----+-----+-----+ tggtccgccccttcagtcgggccccgccgtggggcactgggcagtaggtggcagttgtca	840
841	ccccatgttggaaggcttcacgcccgtattgcgagccttttcgacggcgacgcggggtcgc -----+-----+-----+-----+-----+-----+-----+ ggggtacaaccttcgaagtgcgggctaacgctcggaaaagctgccgctgcgccccagcg	900
901	gcggcaatttntccaacaaggctcagtggaacggcgcgccgatggccgcgcgcagccaggc -----+-----+-----+-----+-----+-----+-----+ cgccgttaaanaggttgttccagtcacctggccgcgcgggtaccggcgcgcgctcggtccg	960
961	atccttggccggaaacacccgcgcccgcacatgatcggccaggatcgtccggcgcgcggc -----+-----+-----+-----+-----+-----+-----+ taggaaccggcctttgtgggcgcgggcgtagtactagccggtcctagcaggccgcggcgcg	1020
1021	gcggcgaggtcgccgcgctcaccggatttgtcaagcaccaggccatcgcgctccgcgac -----+-----+-----+-----+-----+-----+-----+ cgccgcgctccagccggcgagtgggcctaacagttcgtgggtccggtagcgcaggcgctg	1080
1081	ctcgtccgcgtcgtccatgtcgacgatcaggccgttctccatgtcgcggaacagttcgcg -----+-----+-----+-----+-----+-----+-----+ gagcaggcgagcaggtacagctgctagtccggcaagaggtacagcgcttggtcaagcgc	1140
1141	caccggggcggtgttcgatcgatcaccaggcatccggtggccatcgctcggacagggac -----+-----+-----+-----+-----+-----+-----+ gtggccccgccacaagctagctagtgggtccgtaggccaccggtagcggagcctgtccctg	1200
1201	caggaggtgacgaagggtcgggtgaaatagacatgcgctgcgaggcctgcag -----+-----+-----+-----+-----+-----+-----+ gtcctccactgcttcccagccactttatctgtacgcgcacgctccggacgtc	1253

**FIG. 38B**

1	ATGAGACGAGACGTCAACCCGATCCACGCCACCCCTTCTGCAGACCAGACTTGAGGAGATC -----+-----+-----+-----+-----+-----+-----+ TACTCTGCTCTGCAGTTGGGCTAGGTGCGGTGGGAAGACGTCTGGTCTGAACTCCTCTAG	60
61	GCCCAGGGATTCCGGTGCCGTGTCTGCAGCCGCTCGGCCCGGCCATGAGCCATGGCGCGCTG -----+-----+-----+-----+-----+-----+-----+ CGGGTCCCTAAGCCACGGCACAGCGTGGGCGAGCCGGGCCGGTACTCGGTACCGCGCGAC	120
121	TCGTGCGGAAGCGTTTCCGCGGCATGCTGATGCTGCTTGCGGCAGAAGCCTCCCCCGGG -----+-----+-----+-----+-----+-----+-----+ AGCAGCCCGTTCGAAAGGCGCCGTACGACTACGACGAACGCCGTCTTCGGAGCCCGCCC	180
181	GTCTGCGACACGATCGTCGACGCCGCTGCGCGGTGCGAGATGGTGCATGCCGCATCGCTG -----+-----+-----+-----+-----+-----+-----+ CAGACGCTGTGCTAGCAGCTGCGGCGGACGCGCCAGCTCTACCACGTACGGCGTAGCGAC	240
241	ATCTTCGACGACCTGCCCTGCATGGACGATGCCGGGCTGCGCCGCGGCCAGCCCGCGACC -----+-----+-----+-----+-----+-----+-----+ TAGAAGCTGCTGGACGGGACGTACCTGCTACGGCCCGACGCGGCGCCGGTTCGGGCGCTGG	300
301	CATGTGGCGCATGGCGAAAGCCGCGCCGTGCTAGGCGGCATCGCCCTGATCACCGAGGCG -----+-----+-----+-----+-----+-----+-----+ GTACACCGCGTACCGCTTTCGGCGCGGCACGATCCGCCGTAGCGGGACTAGTGGCTCCGC	360
361	ATGGCCCTGCTGGCCGGTGCGCGCGGCGCGTTCGGGCACGGTGCGGGCGCAGCTGGTGGCG -----+-----+-----+-----+-----+-----+-----+ TACCGGGACGACCGGCCACGCGCGCCGCGCAGCCGTGCCACGCCCGCGTTCGACCACGCC	420
421	ATCCTGTCGCGGTCCCTGGGGCCGAGGGCCTGTGCGCCGGCCAGGGCCTGGACCTGCAC -----+-----+-----+-----+-----+-----+-----+ TAGGACAGCGCCAGGGACCCCGGCGTCCCGACACGCGGCCGGTCTTGACCTGGACGTG	480
481	GCGGCCAAGAACGGCGCGGGGGTCTGAACAGGAACAGGACCTGAAGACCGGCGTGCTGTTT -----+-----+-----+-----+-----+-----+-----+ CGCCGGTTCCTTGCCGCGCCCCAGCTTGTCTTGTCTTGACTTCTGGCCGCACGACAAG	540
541	ATCGCCGGGCTGGAGATGCTGGCCGTGATCAAGGAGTTCGACGCCGAGGAGCAGACTCAG -----+-----+-----+-----+-----+-----+-----+ TAGCGGCCCGACCTCTACGACCGGCACTAGTTCTTCAAGCTGCGGCTCCTCGTCTGAGTC	600
601	ATGATCGACTTTGGCCGTGAGCTGGGCCGGGTGTTCCAGTCTTATGACGACCTGCTGGAC -----+-----+-----+-----+-----+-----+-----+ TACTAGCTGAAACCGGCAGTCGACCCGGCCACAAGGTCAGGATACTGCTGGACGACCTG	660

FIG. 39A

```
661 GTTGTGGGCGACCAGGCGGCGCTTGGCAAGGATACCGGTCGCGATGCGGCGGCCCCCGGC 720
-----+-----+-----+-----+-----+-----+
CAACACCCGCTGGTCCGCCGGAACCGTTCCTATGGCCAGCGCTACGCCCGGGGGCCG

721 CCGCGGCGCGGCCTTCTGGCCGTGTCAGACCTGCAGAACGTGTCCCGTCACTATGAGGCC 780
-----+-----+-----+-----+-----+-----+
GGCGCCGCGCCGGAAGACCGGCACAGTCTGGACGTCTTGACAGGGCAGTGATACTCCGG

781 AGCCGCGCCCAGCTGGACGCGATGCTGCGCAGCAAGCGCCTTCAGGCTCCGGAAATCGCG 840
-----+-----+-----+-----+-----+-----+
TCGGCGCGGGTCGACCTGCGCTACGACGCGTCGTTGCGGAAGTCCGAGGCCTTTAGCGC

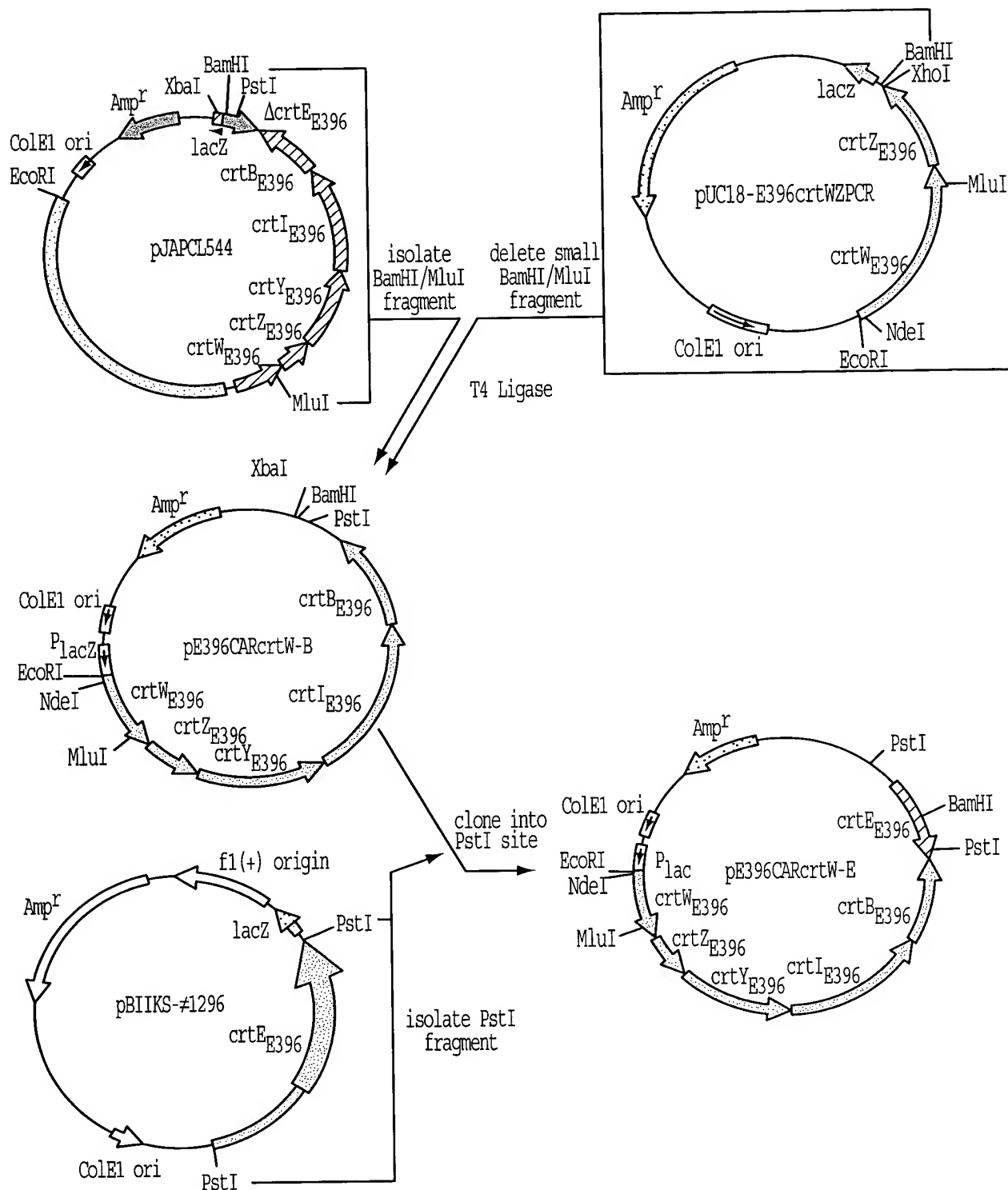
841 GCCCTGCTGGAACGGGTTCTGCCCTACGCCGCGCGGCCTAG
-----+-----+-----+-----+-----+ 882
CGGGACGACCTTGCCCAAGACGGGATGCGGCGCGCGCGGATC
```

FIG. 39B

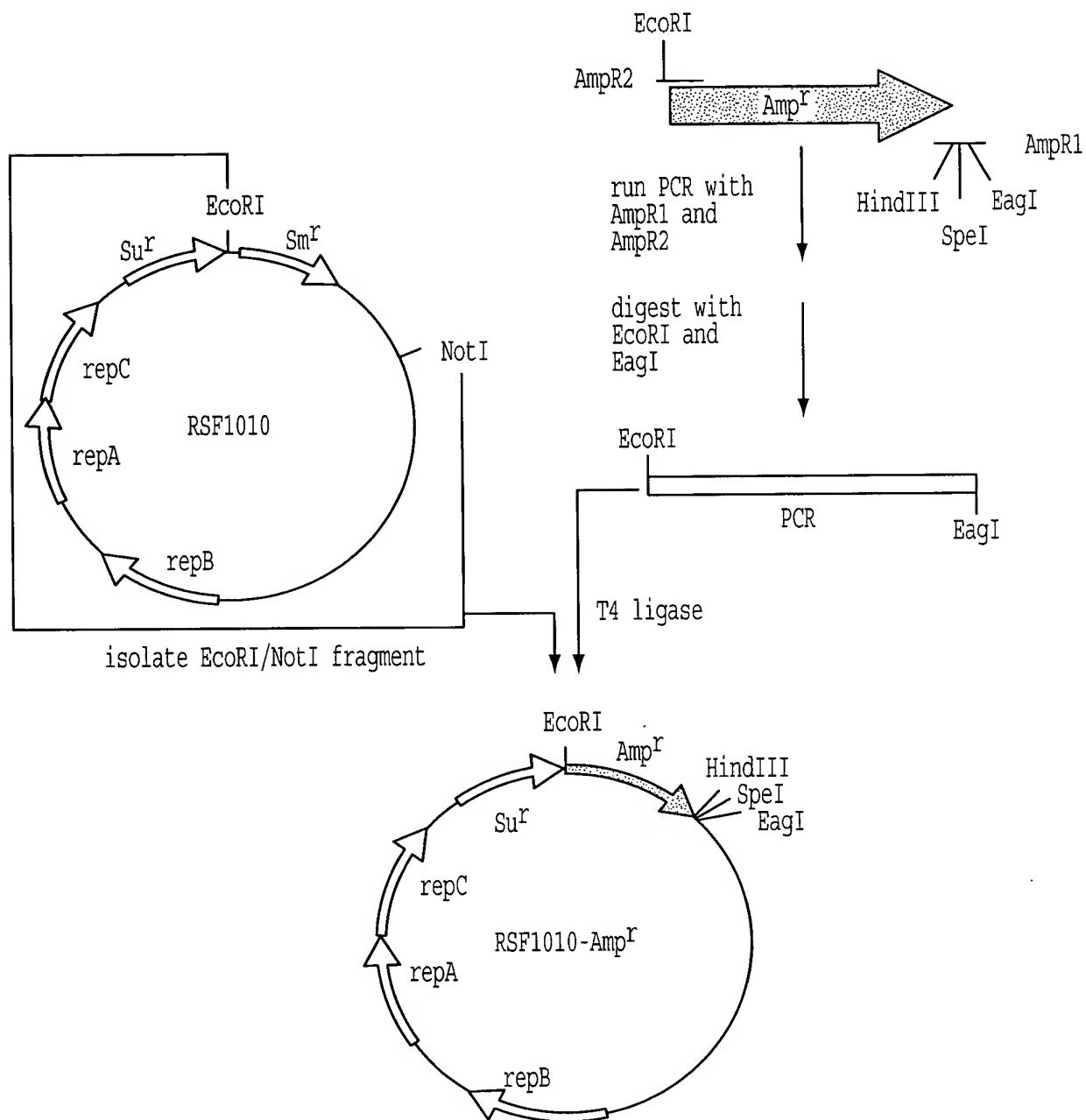
Applicant(s): Luis PASAMONTES and Yuri TSYGANKOV  
Parent Serial No.: 09/920,923  
For: **FERMENTATIVE CAROTENOID  
PRODUCTION**

1 MRRDVNPIHA TLLQTRLEEI AQGFGAVSQP LGPAMSHGAL SSGKRFRGML  
51 MLLAAEASGG VCDTIVDAAC AVEMVHAASL IFDDLPCMDD AGLRRGQPAT  
101 HVAHGESRAV LGGIALITEA MALLAGARGA SGTVRAQLVR ILSRSLGPQG  
151 LCAGQDDLHLH AAKNGAGVEQ EQDLKTGVLF IAGLEMLAVI KEFDAEEQTQ  
201 MIDFGRQLGR VFQSYDDLID VVGDAQALGK DTGRDAAAPG PRRGLLAVSD  
251 LQNVSRHYEA SRAQLDAMLR SKRLQAPEIA ALLERVLPYA ARA\*

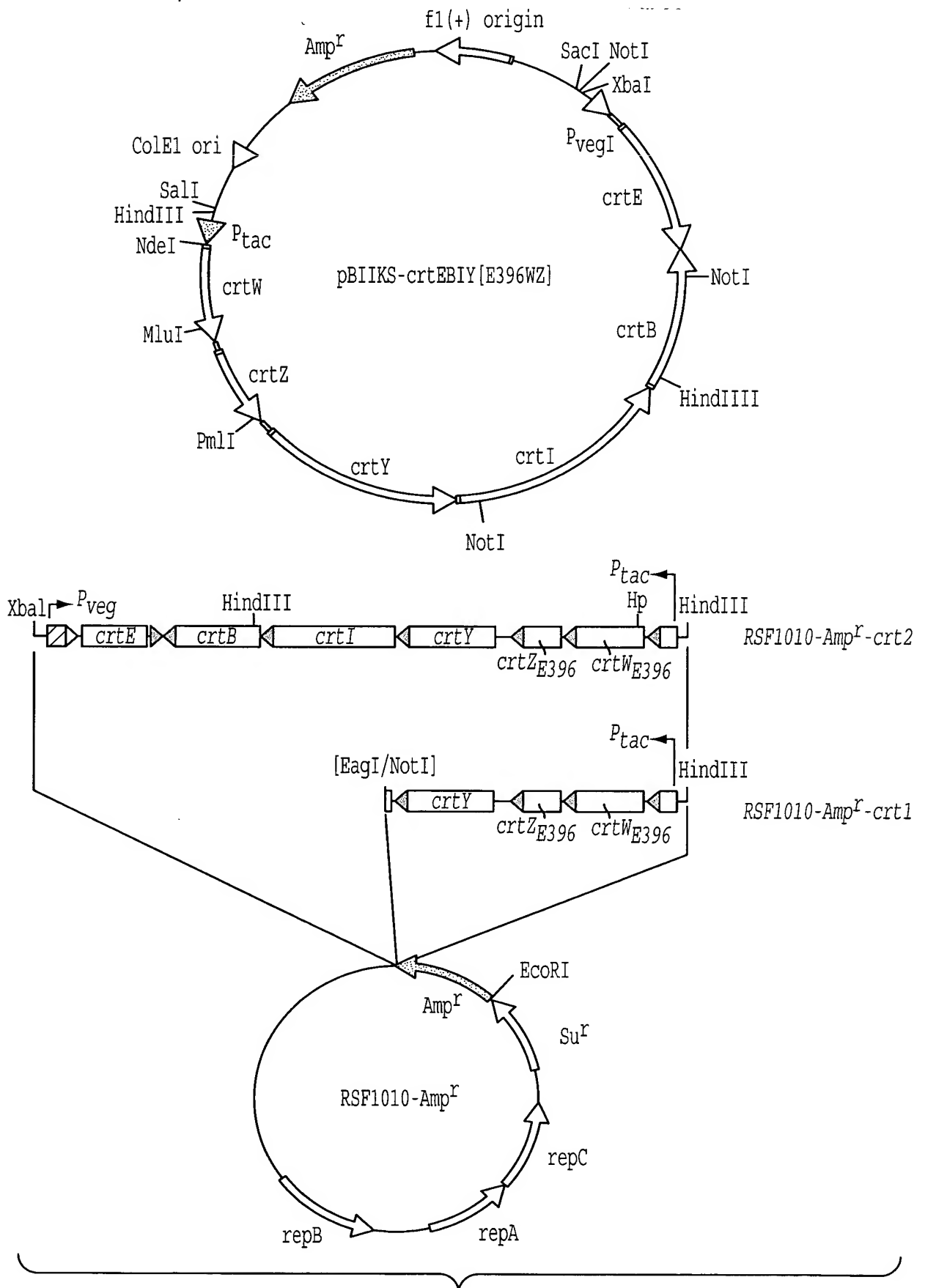
**FIG. 40**



**FIG. 41**



**FIG. 42**



**FIG. 43**